

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2004, 13:11:17 ; Search time 66 Seconds
(without alignments)
1569.204 Million cell updates/sec

Title: US-09-807-148-4
Perfect score: 971
Sequence: 1 BPAVYFKEQFLDGDGWTSRW.....PDNTVEYKIDNSQVSGSL 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	417	1 CRTIC HUMAN	P27797 homo sapien
2	971	100.0	417	2 AAP36116	Aap36116 homo sapi
3	971	100.0	417	3 CAG33351	Cag33351 homo sapi
4	940	96.8	417	1 CRTIC CRIGR	Q8K3h7 cricetus
5	933	96.1	416	1 CRTIC RAT	P18418 rattus norv
6	933	96.1	416	2 AAH62395	Aah62395 rattus no
7	931	95.9	418	1 CRTIC RABIT	P15253 oryctolagus
8	930	95.8	416	1 CRTIC MOUSE	P14211 mus musculu
9	930	95.8	416	2 BAC35852	Bac35852 mus muscu
10	930	95.8	417	1 CRT1 BOVIN	P52193 bos taurus
11	874	90.0	404	2 Q6EE32	Q6ee32 gallus gall
12	843	86.8	413	2 Q7ZW08	Q7zw08 xenopus lae
13	843	86.8	418	2 Q7ZXY3	Q7zxy3 xenopus lae
14	835	86.0	411	2 Q91710	Q91710 xenopus lae
15	820	84.4	416	2 Q6NV76	Q6nvt6 xenopus tro
16	820	84.4	415	2 AAH67917	Aah67917 xenopus t
17	817	84.1	419	2 Q6PF78	Q6pfp8 brachydanio
18	817	84.1	419	2 AAH57469	Aah57469 brachydan
19	804	82.8	405	2 Q26268	Q26268 aplysia cal
20	797	82.1	343	2 Q91711	Q91711 xenopus lae
21	796	82.0	419	2 Q98984	Q98984 rana rugosa
22	785	80.8	417	2 Q9PU01	Q9pu01 brachydanio
23	785	80.8	418	2 Q6NV30	Q6nv30 brachydanio
24	785	80.8	418	2 Q6PE26	Q6pe26 brachydanio
25	785	80.8	418	2 AAH58314	Aah58314 brachydan
26	785	80.8	418	2 AAH68336	Aah68336 brachydan
27	773	79.6	407	2 Q6WSP9	Q6wsp9 dermacentor
28	773	79.6	407	2 Q8G372	Q8g372 dermacentor
29	773	79.6	407	2 AAQ18697	Aaq18697 dermacent
30	769	79.2	423	2 Q7SZM3	Q7szm3 ictalurus p
31	763	78.6	417	2 Q802X3	Q802x3 brachydanio

ALIGNMENTS

RESULT 1

ID	CRTC_HUMAN	STANDARD;	PRT;	417 AA.
DT	P27797;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60) (grp60).			
GN	Name=CALR; Synonyms=CRIC;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92013129; PubMed=1919005;			
RA	Rokeach L.A., Haselby J.A., Meilof J.F., Smeenk R.J., Unnasch T.R.,			
RA	Greene B.M., Hoch S.O.;			
RT	"Characterization of the autoantigen calreticulin.";			
RL	J. Immunol. 147:3031-3039(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90237213; PubMed=2332496;			
RA	McCaulliffe D.P., Lux F.A., Lieu T.S., Sanz I., Hanke J., Newkirk M.M.,			
RA	Bachinski L.L., Itoh Y., Siciliano M.J., Reichlin M., Sontheimer R.D.,			
RA	Capra J.D.;			
RT	"Molecular cloning, expression, and chromosome 19 localization of a			
RT	human Ro/SS-A autoantigen.";			
RL	J. Clin. Invest. 85:1379-1391(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92129342; PubMed=1733953;			
RA	McCaulliffe D.P., Yang Y.S., Wilson J., Sontheimer R.D., Capra J.D.;			
RT	"The 5'-flanking region of the human calreticulin gene shares homology			
RT	with the human GRP78, GRP94, and protein disulfide isomerase			
RT	promoters.";			
RL	J. Biol. Chem. 267:2557-2562(1992).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Liu J., Peng X., Yuan J., Qiang B.;			
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	PubMed=15057824; DOI=10.1038/nature02399;			
RA	Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,			
RA	Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,			
RA	Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,			
RA	Caenepeel S., Carrano A.V., Caille C., Chan Y.M., Christensen M.,			
RA	Cleland C.A., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,			
RA	Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,			
RA	Glavina T., Gomez M., Gonzales E., Groza W., Hammon N., Hawkins T.,			
RA	Raydu L., Ho I., Huang W., Israni S., Jett J., Kacher K., Kimball H.,			
RA	Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,			
RA	Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,			

Q6dl13 brachydanio
Q6wsq2 rhinicephal
Aaq18694 rhiniceph
Q8mwp3 boophilus m
Q16893 amblyomma a
Q6wsq1 haemaphysal
Aaq18695 haemaphys
Q8wsq0 ixodes scap
Q6wsq0 ixodes sc
Aaq18696 ixodes sc
Q6ud79 oncorhynch
Aaarl7084 oncorhyn
Q6u6s0 strongyloce
Q7pqk3 anopheles g
Q8wr36 anopheles g

- RA Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,
 RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,
 RA Rodriguez A., Rogers S., Salazar A., Salazar A., She X., Smith D.,
 RA Slezak T., Solovyev V., Thayer M., Tice H., Tsai M., Ustaszewska A.,
 RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,
 RA Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,
 RA Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
 RA Rubin E.M., Lucas S.M.;
 RA "The DNA sequence and biology of human chromosome 19";
 RL Nature 428:529-535(2004).
 RN [6]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Eye, Pancreas, and Skin;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RN SEQUENCE OF 18-41.
 RP PubMed=3260607;
 RX Lieu T.-S., Newkirk M.M., Capra J.D., Sontheimer R.D.;
 RA "Molecular characterization of human Ro/SS-A antigen. Amino terminal
 RT sequence of the protein moiety of human Ro/SS-A antigen and
 RT immunological activity of a corresponding synthetic peptide";
 RL J. Clin. Invest. 82:96-101(1988).
 RN [8]
 RN SEQUENCE OF 18-36.
 RP MEDLINE=92002034; PubMed=19111778;
 RA Rojiani M.V., Finlay B.B., Gray V., Dedhar S.;
 RA "In vitro interaction of a polypeptide homologous to human Ro/SS-A
 RT antigen (calreticulin) with a highly conserved amino acid sequence in
 RT the cytoplasmic domain of integrin alpha subunits";
 RL Biochemistry 30:9859-9866(1991).
 RN [9]
 RN SEQUENCE OF 18-32.
 RP MEDLINE=90380058; PubMed=2400400;
 RA Krause K.H., Simmerman H.K.B., Jones L.R., Campbell K.P.;
 RA "Sequence similarity of calreticulin with a Ca2+-binding protein
 RT that co-purifies with an Ins(1,4,5)P3-sensitive Ca2+ store in HL-60
 RT cells";
 RL Biochem. J. 270:545-548(1990).
 RN [10]
 RN SEQUENCE OF 18-28.
 RP TISSUE=Liver;
 RX MEDLINE=93162045; PubMed=1286669;
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
 RA Appel R.D., Hughes G.J.;
 RA "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison";
 RL Electrophoresis 13:992-1001(1992).
 RN [11]
 RN PARTIAL SEQUENCE OF 25-34; 56-62; 208-221 AND 273-278.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes";
 RL Electrophoresis 13:960-969(1992).
 RN [12]
 RN SEQUENCE OF 18-27, AND SUBCELLULAR LOCATION.
 RP PubMed=8418194;
 RA Dupuis M., Schaefer E., Krause K.-H., Tschopp J.;
 RT "The calcium-binding protein calreticulin is a major constituent of
 RT lytic granules in cytolytic T lymphocytes";
 RL J. Exp. Med. 177:1-17(1993).
 RN [13]
 RN SEQUENCE OF 18-26.
 RC TISSUE=Colon carcinoma;
 RX MEDLINE=97295306; PubMed=9150948;
 RA Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins";
 RL Electrophoresis 18:605-613(1997).
 RN [14]
 RN FUNCTION.
 RP MEDLINE=95181473; PubMed=7876246;
 RA Nauseef W.M., McCormick S.J., Clark R.A.;
 RT "Calreticulin functions as a molecular chaperone in the biosynthesis
 RT of myeloperoxidase";
 RL J. Biol. Chem. 270:4741-4747(1995).
 RN [15]
 RN SUBCELLULAR LOCATION.
 RP MEDLINE=9287886; PubMed=10358038;
 RA Atosa F.A., de Jesus O., Porto G., Carmo A.M., de Sousa M.;
 RT "Calreticulin is expressed on the cell surface of activated human
 RT peripheral blood T lymphocytes in association with major
 RT histocompatibility complex class I molecules";
 RL J. Biol. Chem. 274:16917-16922(1999).
 RN [16]
 RN FUNCTION, INTERACTION WITH NR3C1, SUBCELLULAR LOCATION, AND MASS
 RP SPECTROMETRY.
 RX MEDLINE=21067064; PubMed=11149926;
 RA Holaska J.M., Black B.E., Love D.C., Hanover J.A., Leszyk J.,
 RA Paschal B.M.;
 RT "Calreticulin is a receptor for nuclear export";
 RL J. Cell Biol. 152:127-140(2001).
 RN [17]
 RN PARTIAL SEQUENCE, MASS SPECTROMETRY, AND DISULFIDE BOND.
 RP TISSUE=Placenta;
 RX MEDLINE=21223009; PubMed=11322874;
 RA Hoejrup P., Roepstorff P., Houen G.;
 RT "Human placental calreticulin characterization of domain structure and
 RT post-translational modifications";
 RL Eur. J. Biochem. 268:2558-2565(2001).
 CC -1- FUNCTION: Molecular calcium binding chaperone promoting folding,
 CC calreticulin/calnexin cycle. This lectin interacts transiently
 CC with almost all of the monoglucosylated glycoproteins that are
 CC synthesized in the ER. Interacts with the DNA-binding domain of
 CC NR3C1 and mediates its nuclear export.
 CC -1- SUBUNIT: Monomer. Interacts with GRP58 (ERP57) and with NR3C1 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen. Also found in
 CC cell surface (T cells), cytosol and extracellular matrix.
 CC Associated with the lytic granules in the cytolytic T-lymphocytes.
 CC -1- DOMAIN: Can be divided into a N-terminal globular domain, a
 CC proline-rich P-domain forming an elongated arm-like structure and
 CC a C-terminal acidic domain. The P-domain binds one molecule of
 CC calcium with high affinity, whereas the acidic C-domain binds
 CC multiple calcium ions with low affinity.
 CC -1- DOMAIN: The interaction with glycans occurs through a binding site
 CC in the globular lectin domain.
 CC -1- DOMAIN: The zinc binding sites are localized to the N-domain.
 CC -1- DOMAIN: Associates with ERP57 through the tip of the extended arm
 CC formed by the P-domain.
 CC -1- MASS SPECTROMETRY: MW=46879; METHOD=MALDI; RANGE=18-417;
 CC NOTE=Ref.16.
 CC -1- SIMILARITY: Belongs to the calreticulin family.

CC -!- CAUTION: Was originally (Ref.2) thought to be the 52 kDa Ro autoantigen.

Query Match 100.0%; Score 971; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 120
DB 78 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 137
QY 121 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 2
AAP36116 PRELIMINARY; PRT; 417 AA.
ID AAP36116
AC AAP36116
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Calreticulin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDs in BD Creator (TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BT007448; AAP36116.1; -;
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 971; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 120
DB 78 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 137
QY 121 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 3
AAP36116 PRELIMINARY; PRT; 417 AA.
ID AAP36116
AC AAP36116
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE CALR protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDs in BD Creator (TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BT007448; AAP36116.1; -;
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 971; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 120
DB 78 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 137
QY 121 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 3
AAP36116 PRELIMINARY; PRT; 417 AA.
ID AAP36116
AC AAP36116
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE CALR protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDs in BD Creator (TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BT007448; AAP36116.1; -;
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 971; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 120
DB 78 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 137
QY 121 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 3
AAP36116 PRELIMINARY; PRT; 417 AA.
ID AAP36116
AC AAP36116
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE CALR protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDs in BD Creator (TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BT007448; AAP36116.1; -;
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 971; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 120
DB 78 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 137
QY 121 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIIFYKGNVKNLINDIRCKDDFTLTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 3
AAP36116 PRELIMINARY; PRT; 417 AA.
ID AAP36116
AC AAP36116
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE CALR protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDs in BD Creator (TM) System Donor
RT vector";
RL Submitted (MAY-2003) to the ENBL/GenBank/DBJ databases.
DR EMBL; BT007448; AAP36116.1; -;
SQ SEQUENCE 417 AA; 48141 MW; BC37C3C0F1054FB2 CRC64;

Query Match 100.0%; Score 971; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 120
DB 78 SASPEPNSKGTLLVQVFTVKHEQNIIDCGGYVKLPNSLDQTDMDGSDSEYNIIMFGPDIC 13

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CC DR ENBL; AY100868; AM48568.1; -.
CC DR HSP; P18418; IHHN.
CC DR InterPro; IPR001580; Calret/calnex.
CC DR InterPro; IPR009169; Calreticulin.
CC DR InterPro; IPR009033; Calret calnex P.
CC DR InterPro; IPR008985; ConA like lec_gl.
CC DR InterPro; IPR00886; ER_target_S.
CC DR Pram; P00262; Calreticulin; 1.
CC DR PIRSF; PIRSF002356; Calreticulin; 1.
CC DR PRINTS; P00626; CALRETICULIN.
CC DR PRODOM; PD001866; Calreticulin; 1.
CC DR PROSITE; PS00803; CALRETICULIN_1; 1.
CC DR PROSITE; PS00804; CALRETICULIN_2; 1.
CC DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC DR PROSITE; PS00014; ER_TARGET; 1.
CC KW Calcium-binding; Chaperone; Endoplasmic reticulum; Lectin;
CC KW Metal-binding; Repeat; Signal; Zinc.
CC FT CHAIN 1 17 By similarity.
CC FT CHAIN 18 417 Calreticulin.
CC FT DOMAIN 18 197 N-domain.
CC FT DOMAIN 198 308 P-domain.
CC FT DOMAIN 309 417 C-domain.
CC FT REPEAT 191 255 4 X approximate repeats.
CC FT REPEAT 210 221 1-1.
CC FT REPEAT 227 238 1-2.
CC FT REPEAT 244 255 1-3.
CC FT REPEAT 259 297 1-4.
CC FT REPEAT 259 297 3 X approximate repeats.
CC FT REPEAT 259 297 2-1.
CC FT REPEAT 273 283 2-2.
CC FT REPEAT 287 297 2-3.
CC FT DOMAIN 351 407 Asp/Glu/Lys-rich.
CC FT DISULFID 105 137 By similarity.
CC FT SITE 414 417 Prevent secretion from ER (Potential).
CC SQ SEQUENCE 417 AA; 48242 MW; D617DA37D14F2D45 CRC64;

Query Match 96.8%; Score 940; DB 1; Length 417;
Best Local Similarity 96.1%; Pred. No. 3.9e-76;
Matches 173; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EBAVFKQFLDGDGWTSEWISKHSDFKVLSSGKFGYDGEKDKLQTSQDARFVAL 60
Db 18 EBAVFKQFLDGDGWTNKRWSKHSDFKVLSSGKFGYDGEKDKLQTSQDARFVAL 77

QY 61 SASFEPFNSKGTLLVQVTFKHEQNDICGGYVKLFNLSLQDTMHDGSEYNINFGPDIC 120
Db 78 SARFEPFNSKGTLLVQVTFKHEQNDICGGYVKLFPGSLDQKMDHGDSEYNINFGPDIC 137

QY 121 GPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSL 180
Db 138 GPGTKKHVIFNYKGNVLINKDIRCKDDETHLYTLVPRDNTYEVKIDNSQVESGSL 197

RESULT 5
CRTC_RAT
ID CRTC_RAT STANDARD; PRT; 416 AA.
AC P18418; P10452;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (CALBP)
DE (Calcium-binding protein 3) (CABP3).
GN Name=Calr;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RX MEDLINE=90370496; PubMed=2395661;
RA Murthy K.K., Banville D., Srikanth C.B., Carrier F., Bell A.,

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RA Holmes C., Patel Y.C.;
RT "Structural homology between the rat calreticulin gene product and the
RL Onchocerca volvulus antigen Ral-1.";
RN Nucleic Acids Res. 18:4933-4933(1990).
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=93202172; PubMed=8453984;
RA Nakamura M., Moriya M., Baba T., Michikawa Y., Yamanobe T., Arai K.,
RA Okinaga S., Kobayashi T.;
RT "An endoplasmic reticulum protein, calreticulin, is transported into
RL the acrosome of rat sperm.";
RN Exp. Cell Res. 205:101-110(1993).
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95181573; PubMed=7876339;
RA Soennichsen B., Fueflekrug J., van Nguyen P., Diekmann W.,
RA Robinson D.G., Mieskes G.;
RT "Retention and retrieval: both mechanisms cooperate to maintain
RL calreticulin in the endoplasmic reticulum.";
RN J. Cell Sci. 107:2705-2717(1994).
RP SEQUENCE OF 270-358 FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RL C2(+) storage compartments (calciosomes) of liver and brain.";
RN Biochem. J. 271:473-480(1990).
RP SEQUENCE OF 18-29.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=9236010; PubMed=1497655;
RA Nakamura M., Michikawa Y., Baba T., Okinaga S., Arai K.;
RT "Calreticulin is present in the acrosome of spermatozoa of rat
RL testis.";
RN Biochem. Biophys. Res. Commun. 186:668-673(1992).
RP SEQUENCE OF 18-32.
RC STRAIN=LEC; TISSUE=Liver;
RX MEDLINE=94072621; PubMed=8251535;
RA Yokoi T., Nagayama S., Kajiura R., Kawaguchi Y., Horiuchi R.,
RA Kamataki T.;
RT "Identification of protein disulfide isomerase and calreticulin as
RL autoantigenic antigens in LEC strain of rats.";
RN Biochim. Biophys. Acta 1158:339-344(1993).
RP TISSUE SPECIFICITY AND SUBCELLULAR LOCATION.
RX MEDLINE=22667233; PubMed=12782144;
RA Somogyi E., Petersson U., Hultenby K., Wendel M.;
RT "Calreticulin--an endoplasmic reticulum protein with calcium-binding
RL activity is also found in the extracellular matrix.";
RN Matrix Biol. 22:179-191(2003).
RP INTERACTION WITH GRP58.
RX PubMed=11842220; DOI=10.1073/pnas.0426990999;
RA Frickel E.M., Riek R., Jelesarov I., Helenius A., Wuthrich K.,
RT "TROSY-NMR reveals interaction between ERp57 and the tip of the
RL calreticulin P-domain.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:1954-1959(2002).
CC -1- FUNCTION: Molecular calcium binding chaperone promoting folding,
CC calreticulin/calnexin cycle. This lectin interacts transiently
CC with almost all of the monoglucosylated glycoproteins that are
CC synthesized in the ER. Interacts with the DNA-binding domain of
CC NR3C1 and mediates its nuclear export (By similarity).

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CC -I- SUBUNIT: Monomer. Interacts with GRP58 (Erp57) and with NR3C1 (By
 CC similarity).

CC -I- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.

CC -I- TISSUE SPECIFICITY: Predentin and odontoblast.

CC -I- DOMAIN: Can be divided into a N-terminal globular domain, a
 CC proline-rich p-domain forming an elongated arm-like structure and
 CC a C-terminal acidic domain. The p-domain binds one molecule of
 CC calcium with high affinity, whereas the acidic C-domain binds
 CC multiple calcium ions with low affinity (By similarity).

CC -I- DOMAIN: The interaction with glycans occurs through a binding site
 CC in the globular lectin domain (By similarity).

CC -I- DOMAIN: The zinc binding sites are localized to the N-domain (By
 CC similarity).

CC -I- DOMAIN: Associates with Erp57 through the tip of the extended arm
 CC formed by the p-domain (By similarity).

CC -I- SIMILARITY: Belongs to the calreticulin family.

CC -I- CAUTION: Was originally (Ref.2) thought to be D-beta-
 CC hydroxybutyrate dehydrogenase.

CC -----

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 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; D78308; BAA11345.1; --

DR EMBL; X53363; CAA37446.1; --

DR EMBL; X13702; CAA31987.1; ALT_SEQ.

DR EMBL; X79327; CAA55890.1; --

DR PIR; JH0819; JH0819.

DR PDB; 1HHN; NMR; A=205-305.

DR PDB; 1K91; NMR; A=237-273.

DR PDB; 1K9C; NMR; A=205-278.

DR RGD; 620288; Calr.

DR InterPro; IPR001580; Calret/calnex.

DR InterPro; IPR009169; Calreticulin.

DR InterPro; IPR009033; Calret/calnex_P.

DR InterPro; IPR008985; ConA like lec_gl.

DR InterPro; IPR000886; ER target_S.

DR Pfam; PF00262; Calreticulin; 1.

DR Pfam; PF002356; Calreticulin; 1.

DR PRINTS; PR0626; CALRETICULIN.

DR ProDom; PD001866; Calreticulin; 1.

DR PROSITE; PS00803; CALRETICULIN_1; 1.

DR PROSITE; PS00804; CALRETICULIN_2; 1.

DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.

DR PROSITE; PS00014; ER_TARGET; 1.

DR 3D-structure; Calcium-binding; Chaperone; Direct protein sequencing;
 KW Endoplasmic reticulum; Lectin; Metal-binding; Repeat; Signal; Zinc.

FT SIGNAL 1 17

FT CHAIN 18 416 Calreticulin.

FT DOMAIN 18 197 N-domain.

FT DOMAIN 198 308 P-domain.

FT DOMAIN 309 416 C-domain.

FT DOMAIN 191 255 4 X approximate repeats.

FT REPEAT 191 202 1-1.

FT REPEAT 210 221 1-2.

FT REPEAT 227 238 1-3.

FT REPEAT 244 255 1-4.

FT DOMAIN 259 297 3 X approximate repeats.

FT REPEAT 259 269 2-1.

FT REPEAT 273 283 2-2.

FT REPEAT 287 297 2-3.

FT DOMAIN 351 407 Asp/Glu/Lys-rich.

FT DISULFID 105 137 By similarity.

FT SITE 413 416 Prevent secretion from ER.

FT STRAND 208 208

FT TURN 212 213

FT TURN 221 222

FT STRAND 224 225

FT TURN 235 236

FT STRAND 241 243

FT TURN 245 246

FT TURN 251 252

FT HELIX 255 258

FT STRAND 265 267

FT TURN 269 270

FT STRAND 280 281

FT STRAND 294 294

FT TURN 297 298

SQ SEQUENCE 416 AA; 47995 MW; 2B6713CED31A2970 CRC64;

Query Match 96.1%; Score 933; DB 1; Length 416;

Best Local Similarity 94.4%; Pred. No. 1.7e-75;

Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 BPAYVKEQFDGQWTSRWIESKHSDFGKFLVSSCKFYGDESKDKGLQTSQDARFYAL 60

DB 18 DPAIYFKEQFDGDAWNRWVESKHSDFGKFLVSSCKFYGDESKDKGLQTSQDARFYAL 77

QY 61 SASPEPSNKGQTLVVQFTVKHEQNIDCGGYVKLFPSNLDQDTHGDSSEYNINFGPDIC 120

DB 78 SARPEPSNKGQTLVVQFTVKHEQNIDCGGYVKLFPGGLDQKMHGDSSEYNINFGPDIC 137

QY 121 GPGTKKHVIFPNYKGNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180

DB 138 GPGTKKHVIFPNYKGNVLINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 6

AAH62395 PRELIMINARY; PRT; 416 AA.

ID AAH62395

AC AAH62395

DT 02-MAR-2004 (TRENBLrel. 27, Created)

DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)

DE Calreticulin.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

EX MEDLINE=22389257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Prostate;

RA Strausberg R.;

RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC062395; AAH62395.1; --

SQ SEQUENCE 416 AA; 47995 MW; 2E6713CED31A2970 CRC64;

Query Match 96.1%; Score 933; DB 2; Length 416;

Best Local Similarity 94.4%; Pred. No. 1.7e-75;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPVAYEKEQFLDGDGHTSWIWSKHSDFGKFLVSGKTYGDBEYKDLQISQDARFYAL 60
DB DPAYEKEQFLDGDGHTSWIWSKHSDFGKFLVSGKTYGDBEYKDLQISQDARFYAL 77

QY 61 SASFEFNSKQTLVQVTFVKEHQNDICGGYVKKLPNLSLQDTDMHGDSYNNMFGPDIC 120
DB SARFEFNSKQTLVQVTFVKEHQNDICGGYVKKLPNLSLQDTDMHGDSYNNMFGPDIC 137

QY 121 GPCTKKVHVFYKGNVNLINKDIRCKDDEFFHLVTLVIRPNTYEVKIDNSQVSGSLE 180
DB GPCTKKVHVFYKGNVNLINKDIRCKDDEFFHLVTLVIRPNTYEVKIDNSQVSGSLE 197

RESULT 7

CRTC-RABIT STANDARD; PRT; 418 AA.

AC P15253;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (BRp60).
GN Name=CAUR;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagonomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_SEQUENCE FROM N.A.
RP TISSUE=slow-twitch skeletal muscle;
RC MEDLINE=90094320; PubMed=2600080;
RA Fliegel L., Burns K., MacLennan D.H., Reithmeier R.A.F., Michalak M.;
RT "Molecular cloning of the high affinity calcium-binding protein
RT (calreticulin) of skeletal muscle sarcoplasmic reticulum";
RL J. Biol. Chem. 264:21522-21528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=fast-twitch skeletal muscle;
RX MEDLINE=91282795; PubMed=2059224;
RA Fliegel L., Michalak M.;
RT "Fast-twitch and slow-twitch skeletal muscles express the same isoform
RT of calreticulin";
RL Biochem. Biophys. Res. Commun. 177:979-984(1991).
RN [3]
RP SEQUENCE OF 18-36.
RX MEDLINE=91054414; PubMed=2241926;
RA Treves S., de Mattei M., Lanfredi M., Villa A., Green N.M.,
RA MacLennan D.H., Meldolesi J., Pozzan T.;
RT "Calreticulin is a candidate for a calsequestrin-like function in
RT Ca2(+)-storage compartments (calciosomes) of liver and brain";
RL Biochem. J. 271:473-480(1990).
RN [4]
RP SEQUENCE OF 18-46.
RX MEDLINE=91201375; PubMed=2016321;
RA Milner R.E., Baksh S., Shenanko C., Carpenter M.R., Smillie L.,
RA Vance J.E., Opas M., Michalak M.;
RT "Calreticulin, and not calsequestrin, is the major calcium binding
RT protein of smooth muscle sarcoplasmic reticulum and liver endoplasmic
RT reticulum";
RL J. Biol. Chem. 266:7155-7165(1991).
RN [5]
RP PARTIAL SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=92002038; PubMed=1911780;
RA Guan S., Falick A.M., Williams D.E., Cashman J.R.;
RT "Evidence for complex formation between rabbit lung flavin-containing
RT monooxygenase and calreticulin";
RL Biochemistry 30:9892-9900(1991).
RN [6]
RP FUNCTION.
RX MEDLINE=20050566; PubMed=10581245;

RA Saito Y., Ihara Y., Leach M.R., Cohen-Doyle M.F., Williams D.B.;
RT "Calreticulin functions in vitro as a molecular chaperone for both
RT glycosylated and non-glycosylated proteins.";
RL EMBL J. 18:6718-6729(1999).
RN [7]
RP ZINC-BINDING DOMAIN.
RX PubMed=8521965; DOI=10.1016/0014-5793(95)01246-4;
RA Baksh S., Spamer C., Heilmann C., Michalak M.;
RT "Identification of the Zn2+ binding region in calreticulin.";
RL FEBS Lett. 376:53-57(1995).
RN [8]
RP MUTAGENESIS OF HIS-170.
RX PubMed=14522955; DOI=10.1074/jbc.M309497200;
RA Guo L., Groenendyk J., Papp S., Dabrowska M., Knoblauch B., Kay C.,
RA Parker J.M., Opas M., Michalak M.;
RT "Identification of an N-domain histidine essential for chaperone
RT function in calreticulin.";
RL J. Biol. Chem. 278:50645-50653(2003).
CC -1- FUNCTION: Molecular calcium binding chaperone promoting folding,
CC oligomeric assembly and quality control in the ER via the
CC calreticulin/calnexin cycle. This lectin interacts transiently
CC with almost all of the monoglucosylated glycoproteins that are
CC synthesized in the ER. Interacts with the DNA-binding domain of
CC NR3C1 and mediates its nuclear export (By similarity).
CC -1- SUBUNIT: Monomer. Interacts with GRP58 (ERP57) and with NR3C1 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- DOMAIN: Can be divided into a N-terminal globular domain, a
CC proline-rich P-domain forming an elongated arm-like structure and
CC a C-terminal acidic domain. The P-domain binds one molecule of
CC calcium with high affinity, whereas the acidic C-domain binds
CC multiple calcium ions with low affinity (By similarity).
CC -1- DOMAIN: The interaction with glycans occurs through a binding site
CC in the globular lectin domain (By similarity).
CC -1- DOMAIN: The zinc binding sites are localized to the N-domain.
CC -1- DOMAIN: Associates with ERp57 through the tip of the extended arm
CC formed by the P-domain (By similarity).
CC -1- SIMILARITY: Belongs to the calreticulin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J051138; AAA31188.1; -.
CC PIR; A34154; A34154.
CC PIR; C33208; C33208.
CC PIR; S13046; S13046.
CC HSP; P18418; I1891.
CC InterPro; IPR001580; Calret/calnex.
CC InterPro; IPR009169; Calreticulin.
CC InterPro; IPR009033; Calret calnex P.
CC InterPro; IPR008985; Cona like lec_g1.
CC Pfam; PF00262; Calreticulin_1.
CC PRINTS; PIRSF002356; Calreticulin; 1.
CC PROSITE; PS00626; CALRETICULIN.
CC PROSITE; PS00803; CALRETICULIN_1; 1.
CC PROSITE; PS00804; CALRETICULIN_2; 1.
CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
CC PROSITE; PS0014; ER_TARGET; 1.
CC Calcium-binding; Chaperone; Direct protein sequencing;
CC Endoplasmic reticulum; Lectin; Metal-binding; Repeat; Signal; Zinc.
FT SIGNAL 1 17
FT CHAIN 18 418 Calreticulin.
FT DOMAIN 18 197 N-domain.
FT DOMAIN 198 308 P-domain.
FT DOMAIN 309 418 C-domain.
FT DOMAIN 191 255 4 X approximate repeats.

FT REPEAT 191 202 1-1.
 FT REPEAT 210 221 1-2.
 FT REPEAT 227 238 1-3.
 FT REPEAT 244 255 1-4.
 FT DOMAIN 259 267 3 X approximate repeats.
 FT REPEAT 269 279 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 287 297 2-3.
 FT DOMAIN 351 408 Asp/Glu/Lys-rich.
 FT DISULFID 105 137 By similarity.
 FT SITE 415 418 Prevent secretion from ER.
 FT VARIANT 35 35 E -> D.
 FT MUTAGEN 170 170 E->A: Loss of activity.
 FT CONFLICT 190 90 P -> T (in Ref. 5).
 SQ SEQUENCE 418 AA; 48275 MW; B6082B689DC763A6 CRC64;

Query Match 95.9%; Score 931; DB 1; Length 418;
 Best Local Similarity 95.6%; Pred. No. 2.5e-75;
 Matches 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 EPVYFKQQLDGGWTSRIEYKHKSDFGKFLVSSGKFGYDEKDKGLQTSODARFYAL 60
 DB 18 EPVYFKQQLDGGWTSRIEYKHKSDFGKFLVSSGKFGYDEKDKGLQTSODARFYAL 77

QY 61 SASFEPSPKQQLVQFTVKHEQNIDCGGYVKLPNSLDQDMHGDSEYNIMFGPDIC 120
 DB 78 SASFEPSPKQQLVQFTVKHEQNIDCGGYVKLPAGLDQDMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIFNYGKGNLVKINDIRCKDBFTHLYLIVRPDNTYEVKIDNSQVSGSLE 180
 DB 138 GPGTKKVHVIFNYGKGNLVKINDIRCKDBFTHLYLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 8

CRTC_MOUSE STANDARD; PRT; 416 AA.

ID CRTC_MOUSE
 AC P14211;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERP60).
 GN Name=Calr;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-48 AND 129-161.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=90059955; PubMed=2583110;
 RA Smith M.J., Koch G.L.E.;
 RT "Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a major calcium binding ER/SR protein.";
 RL EMBO J. 8:3581-3586(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93013037; PubMed=1398135;
 RA Mazzarella R.A., Gold P., Cunningham M., Green M.;
 RT "Determination of the sequence of an expressible cDNA clone encoding ERp60/calregulin by the use of a novel nested set method.";
 RL Gene 120:217-225(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nakaide I., Osato N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Naita K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N-3; TISSUE=Mammary gland;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Schnerth A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 18-38.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins using
 preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 RN [6]
 RP SUBCELLULAR LOCATION.
 RX PubMed=8418194;
 RA Dupuis M., Schaefer E., Krause K.-H., Tschopp J.;
 RT "The calcium-binding protein calreticulin is a major constituent of
 lytic granules in cytolytic T lymphocytes.";
 RL J. Exp. Med. 177:1-7(1993).
 CC -!- FUNCTION: Molecular calcium binding chaperone promoting folding,
 CC oligomeric assembly and quality control in the ER via the
 CC calreticulin/calnexin cycle. This lectin interacts transiently
 CC with almost all of the monoglucosylated glycoproteins that are
 CC synthesized in the ER. Interacts with the DNA-binding domain of
 CC NR3C1 and mediates its nuclear export (by similarity).
 CC -!- SUBUNIT: Monomer. Interacts with GRP58 (ERP57) and with NR3C1 (by
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen. Associated with
 CC the lytic granules in the cytolytic T-lymphocytes.
 CC -!- DOMAIN: Can be divided into a N-terminal globular domain, a
 CC proline-rich P-domain forming an elongated arm-like structure and
 CC a C-terminal acidic domain. The P-domain binds one molecule of

CC calcium with high affinity, whereas the acidic C-domain binds
 CC multiple calcium ions with low affinity (By similarity).
 CC -|- DOMAIN: The interaction with glycans occurs through a binding site
 CC in the globular lectin domain (By similarity).
 CC -|- DOMAIN: The zinc binding sites are localized to the N-domain (By
 CC similarity).
 CC -|- DOMAIN: Associates with ERp57 through the tip of the extended arm
 CC formed by the P-domain (By similarity).
 CC -|- SIMILARITY: Belongs to the calreticulin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X14926; CAA33053.1; -;
 CC EMBL; M92988; AAA37569.1; -;
 CC EMBL; AK075605; BAC35852.1; -;
 CC EMBL; BC003453; AA03453.1; -;
 CC PIR; S06763; S06763.
 CC HSP; P18418; IHHN.
 CC SWISS-2DPAGE; P14211; MOUSE.
 CC MGD; MGI:88252; Calr.
 CC GO; GO:0005509; F:calcium ion binding; IDA.
 CC InterPro; IPR001580; Calret/calnex.
 CC InterPro; IPR009169; Calreticulin.
 CC InterPro; IPR009033; Calret calnex P.
 CC InterPro; IPR008985; ConA like lec_gl.
 CC InterPro; IPR000886; ER target_S.
 CC Pfam; PF00262; Calreticulin; 1.
 CC PIRSF; PIRSF002356; Calreticulin; 1.
 CC PRINTS; PR00626; CALRETICULIN.
 CC ProDom; PD001866; Calreticulin; 1.
 CC PROSITE; PS00803; CALRETICULIN 1; 1.
 CC PROSITE; PS00804; CALRETICULIN 2; 1.
 CC PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
 CC PROSITE; PS00014; ER_TARGET; 1.
 CC Calcium-binding; Chaperone; Direct protein sequencing;
 KW Endoplasmic reticulum; Lectin; Metal-binding; Repeat; Signal; zinc.
 FT SIGNAL 1 17
 FT CHAIN 18 416 Calreticulin.
 FT DOMAIN 18 197 N-domain.
 FT DOMAIN 198 308 P-domain.
 FT DOMAIN 309 416 C-domain.
 FT REPEAT 191 255 4 X approximate repeats.
 FT REPEAT 210 221 1-1.
 FT REPEAT 227 238 1-2.
 FT REPEAT 244 255 1-3.
 FT REPEAT 259 297 1-4.
 FT REPEAT 259 297 3 X approximate repeats.
 FT REPEAT 273 283 2-1.
 FT REPEAT 273 283 2-2.
 FT REPEAT 273 283 2-3.
 FT DOMAIN 351 407 Asp/Glu/Lys-rich.
 FT DISULFID 105 137 By similarity.
 FT SITE 413 416 Prevent secretion from ER.
 FT SEQUENCE 416 AA; 47994 MW; 24C03B00913408D8 CRC64;
 Query Match 95.8%; Score 930; DB 1; Length 416;
 Best Local Similarity 94.4%; Pred. No. 3.1e-75;
 Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 EPAYVFEQFLDGDGWTSTWIESKHSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFVAL 60
 Db 18 DPAIVFEQFLDGDGWTSTWIESKHSDFGKFLVSSGKFGYDGEKDKGLQTSQDARFVAL 77
 QY 61 SASFPFNSKGTLLVQVFTVQVTEHQNDICGGGYVLFNPSLDQTDVHGDSYNNIFGPDIC 120
 Db 78 SAKFPFNSKGTLLVQVFTVQVTEHQNDICGGGYVLFNPSLDQTDVHGDSYNNIFGPDIC 137

QY 121 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFFTHLYTLIVRPDNTYEVKIDNSQVSSGLE 180
 Db 138 GPGTKKVHVIFNYKGNVLINKDIRCKDDEFFTHLYTLIVRPDNTYEVKIDNSQVSSGLE 197
 RESULT 9
 BAC35852
 ID BAC35852 PRELIMINARY; PRT; 416 AA.
 AC BAC35852;
 DT 14-APR-2004 (TrEMBLrel. 27, Created)
 DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
 DE Adult male brain cDNA, RIKEN full-length enriched library,
 DE clone:0710001D13 product:calreticulin, full insert sequence.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCEL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=21085660; PubMed=11217851;
 RA RIKEN PANTOM Consortium;
 RA "Functional annotation of a full-length mouse cDNA collection."
 RT Nature 409:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu N., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=20493374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu N., Sugahara Y., Itoh M.,
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Kitsumai T., Tashiro H., Itoh M.,
 RA Konno H., Akiyama J., Nishi K., Kitsumai T., Nishine T., Hazada A.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Kashiwagi K.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Brain;
 RC Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanaoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kuribara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,


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--!- SIMILARITY: Belongs to the calreticulin family.
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EMBL; AB067897; BAB86913.1; --
HSSP; P18418; IK91.
DR DR InterPro; IPR001580; Calret/calnexin.
DR DR InterPro; IPR009169; Calreticulatin.
DR DR InterPro; IPR009033; Calret_calnex_P.
DR DR InterPro; IPR008985; ConA_like_lec_gl.
DR DR InterPro; IPR000886; ER_target_S.
DR DR Pfam; PF00262; Calreticulin_1.
DR DR PIRSF; PIRSFO02356; Calreticulin; 1.
DR DR PRINTS; PR00626; CALRETICULIN.
DR DR ProDom; PD001866; Calreticulin; 1.
DR DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR DR PROSITE; PS00014; ER_TARGET; 1.
KW Calcium-binding; Chaperone; Direct protein sequencing;
KW Endoplasmic reticulum; Glycoprotein; Lectin; Metal-binding; Repeat; Signal; Zinc.
FT SIGNAL 1 17 Calreticulin, brain isoform 1.
FT FT CHAIN 18 417 N-domain.
FT FT DOMAIN 18 197 P-domain.
FT FT DOMAIN 198 308 C-domain.
FT FT DOMAIN 309 417 P-domain.
FT FT DOMAIN 191 255 4 X approximate repeats.
FT FT REPEAT 191 202 1-1.
FT FT REPEAT 201 221 1-2.
FT FT REPEAT 221 238 1-3.
FT FT REPEAT 238 255 1-4.
FT FT REPEAT 244 297 3 X approximate repeats.
FT FT DOMAIN 259 269 2-1.
FT FT REPEAT 269 283 2-2.
FT FT REPEAT 283 297 2-3.
FT FT DOMAIN 351 407 Asp/Glu/Lys-rich.
FT FT DISULFID 137 163 N-linked (GlcNAc...),
FT FT CARBOHYD 179 179 Prevent secretion from ER (Potential).
FT SITE 414 417
SQ SEQUENCE 417 AA; 48038 MW; 7BF812C7B5417BE9 CRC64;

Query Match          95.8%; Score 930; DB 1; Length 417;
Best Local Similarity 95.0%; Pred. No. 3.le-75;
Matches 171; Conservative    3; Mismatches   6; Indels      0; Gaps     0;

QY Q 1 EPAYFKEQFLDDGGWTSRWIESKHKSDFGKFVLSGKYVGDEKDKGQTQSODARFYAL 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB DPTVFVKEFQLDDGGWTERTWIESKHKRPDFGFVLSGKYFGQEKKDGKTQSODARFYAL 77

QY Q 61 SASPEPPSNKQTLLVOFTVKHEONIDCGGYGVKLFPNSLDQDTDMHGDSSEYNIMFGPDIC 120
DB SARPEPPSNKQTLLVOFTVKHEONIDCGGYGVKLFPAGLDQTDMHGDSEYNIMEFGPDIC 137

QY Q 121 GSGTKKVHVIFNYXGNVLINKOIRCDDFEHTLYTLVRPNPTYEVKIDNQQVSGLSL 180
DB GSGTKKVHVIFNYXGNVLINKOIRCDDFEHTLYTLVRPNNTYEVDKNQNQQVSGLSL 197

RESULT 11
QID ID PRELIMINARY; PRT; 404 AA.
AC AC Q6EE32;
DT DT 01-OCT-2004 (TriEBMrel. 28, Created)
DT DT 01-OCT-2004 (TriEBMrel. 28, Last sequence update)
DT DT 01-OCT-2004 (TriEBMrel. 28, Last annotation update)
DE DE Calreticulin [Fragment].
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SEQUENCE FROM N.A.
RP TSUUE=Embryo;
RC MEDLINE=23341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -/- SIMILARITY: Belongs to the calreticulin family.
DR EMBL; BCO46699; AAH46699.1; -
DR HSP; P18418; IK91.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR InterPro; IPRO01580; Calret/calnex.
DR InterPro; IPRO09169; Calret/calnex.
DR InterPro; IPRO09033; Calret.calnex.P.
DR InterPro; IPRO00886; ER.target_S_g1.
DR PIRSF; PIRSF002356; calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Chaperone; Endoplasmic reticulum.
SQ SEQUENCE 413 AA; 48521 MW; DE002F8F0523772B CRC64;

Query Match 86.8%; Score 843; DB 2; Length 413;
Best Local Similarity 84.4%; P-Ed. No. 2.1e-67;
Matches 152; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 EBAVYFKEQFLDGDGWTSRWISKKHSDFGKVLSSGKFYDEEKKDKGLQTSQDARFYAL 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19 EBAVYFKEFSQDGDGTQWSEKHSKSDYGFKLSAGKFYDGSEKDKGLQTSQDARFYAM 78
QY 61 SASFPFNSKGTQVLVQFPTVXHEQNIQDGGGVYKVLFPNSLDQTDHMGDSSEYNIIMFGPDIC 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 SRFPSFNSKDTLVLIQPSVKHEQNIQDGGGVYKVLFPADLEQTEMHGESEYNIIMFGPDIC 138
QY 121 GPGTKKKVHVIFNYKGNVLINKIDCKDDFTHLYTLVIRPDNTVEYKIDNSQVSGSLE 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 GPGTKKKVHVIFQYKKKNLQINKIDCKDDSFTHLYTLVIRPDNTVEYKIDNSKVSGSLE 198

RESULT 13
Q7ZYX3 Q7ZYX3 PRELIMINARY; PRT; 418 AA.
ID Q7ZYX3
AC Q7ZYX3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
DE Crc-prov protein.
DE OS Xenopus laevis (African clawed frog).
DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
DE OC Xenopodinae; Xenopus.
DE NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA MEDLINE=23388257; PubMed=12477932;
RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Haiech F.,
RA Diachenko I., Vassine K., Farrow A.A., Eick C.M.,
RA
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC MEDLINE=22341132; PubMed=12454917;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC Klein S., Strausberg R.,
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the calreticulin family.
DR EMBL; BC040668; AA44068.1; -;
DR HSP; P18418; Ix91.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:000514; F:calcium ion storage activity; IEA.
DR GO; GO:0003754; F:chaperone activity; IEA.
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR009169; Calreticulin.
DR InterPro; IPR009033; Calret/calnex.P.
DR InterPro; IPR008985; ConA like lec_gl.
DR PIRSF; PIRSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Chaperone; Endoplasmic reticulum.
SQ SEQUENCE 418 AA; 49028 MW; 731C1C9AA03F9A53 CRC64;
Query Match 86.8%; Score 843; DB 2; Length 418;
Best Local Similarity 84.4%; Pred. No. 2.1e-67;
Matches 152; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
QY 1 EPAYVKEQFLDGGWTSRWIESKHGDFGVLSGKFGYDSEKDKGLQTSQDARFYAL 60
Db 19 EPAYVKEEFDDGGWTSRWIESKHGDFGVLSGKFGYDSEKDKGLQTSQDARFYAM 78
QY 61 SASPEFFSNKQDTLVVQFTVKHEQNIIDCGGYVKLPFNSLDQTMHGDSEYNIMFGPDIC 120
Db 79 SSRFDSFNSKQDTLVVQFVSVKHEQNIIDCGGYVKLPFPAALQETEMHGESEYNIMFGPDIC 138
QY 121 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLIVRPDNTYEVKIDNSOVESGSLE 180
Db 139 GPPTKKVHVIFQYKKKLNQINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSOVESGSLE 198
RESULT 14
Q91710 PRELIMINARY; PRT; 411 AA.
ID Q91710
AC Q91710;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Calreticulin precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=CNS;
RC Triebes S., Zorzato F., Pozzan T.,
RT "Identification of calreticulin isoform in the CNS";
RL Biochem. J. 0:0-0(0).
RN [2]
RN SEQUENCE FROM N.A.
RP TISSUE=CNS;
RC Triebes S.,
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the calreticulin family.
DR EMBL; X67597; CAA47866.1; -;
DR PIR; S29129; S29129.
DR GO; GO:000514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR009033; Calret/calnex.P.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR00886; ER_target_S.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR ProDom; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 2.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Chaperone; Endoplasmic reticulum; Signal.
FT NON_TER 1
FT SIGNAL 12 Potential.
FT CHAIN 13 411 calreticulin.
SQ SEQUENCE 411 AA; 48344 MW; 831DA66E30EBEFA CRC64;
Query Match 86.0%; Score 835; DB 2; Length 411;
Best Local Similarity 83.9%; Pred. No. 1.1e-66;
Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
QY 1 EPAYVKEQFLDGGWTSRWIESKHGDFGVLSGKFGYDSEKDKGLQTSQDARFYAL 60
Db 13 EPAYVKEEFDDGGWTSRWIESKHGDFGVLSGKFGYDSEKDKGLQTSQDARFYAM 72
QY 61 SASPEFFSNKQDTLVVQFTVKHEQNIIDCGGYVKLPFNSLDQTMHGDSEYNIMFGPDIC 120
Db 73 SSRFDSFNSKQDTLVVQFVSVKHEQNIIDCGGYVKLPFPAALQETEMHGESEYNIMFGPDIC 132
QY 121 GPGTKKHVIFNYKGNVINKIRCKDDETHLYTLIVRPDNTYEVKIDNSOVESGSLE 180
Db 133 GPPTKKVHVIFQYKKKLNQINKIRCKDDSFTHLYTLIVRPDNTYEVKIDNSOVESGSLE 192
RESULT 15
Q6NVT6 PRELIMINARY; PRT; 416 AA.
ID Q6NVT6
AC Q6NVT6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC69541.
GN Name=MGC69541;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
CX NCBI_TaxID=8364;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Embryo;

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RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC067917; AAH67917.1; -
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR009169; Calreticulin.
DR InterPro; IPR008985; ConA like lec_g1.
DR InterPro; IPR008886; ER_target_S.
DR Pfam; PF00462; Calreticulin; 1.
DR FIRST; F1RSF002356; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00804; CALRETICULIN_2; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 416 AA; 48793 MW; A18E5526796BD850 CRC64;

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Query Match      84.4%; Score 820; DB 2; Length 416;
Best Local Similarity 81.7%; Pred No. 2.4e-65;
Matches 147; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

QY 1 EPATYFKQFLDGDGWTGRWIESKHSDFGKFLVSSGKFGDEKDKGLQTSQDARFYAL 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
19 DPAVYLKEEFADGDGWSQRWVESKHSDYGNKFLSAGKFGDAEKDKGLQTSQDARFYAL 78
QY 61 SASPEFPENKGGTLVQFTVKEQNIDCGGGYVKLFNPSLDOTMHDGSEYNIMFGPDIC 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 STRFDSFNKDKTLVIQFSVHQEINIDCGGGYVKLFFPAELQSEHGESEYNIMFGPDIC 138
QY 121 GPGTKKXHVIFNYKGNVLYNKDKRCKDEFTHLTYLTVRPDNTYEVKIDNSQVESGSLE 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
139 GPPTKKXHVIFQYKKKNQINKDKIRCRDSDSTHLTYLTVRPDNTYEVKIDNSKVESGSLE 198

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Search completed: October 15, 2004, 13:12:33
Job time : 68 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2004, 13:11:17 ; Search time 15 Seconds
(without alignments)
1154.601 Million cell updates/sec

Title: US-09-807-148-4
Perfect score: 971
Sequence: 1 ENAVYKEQFLDGDGWTNRW.....PDNTVEVKIDNSQVSGSL 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	417	A37047	calreticulin precu
2	933	96.1	416	JH0819	calreticulin precu
3	931	95.9	418	A34154	calreticulin precu
4	930	95.8	400	S43176	calreticulin, brai
5	930	95.8	416	S06763	calreticulin, precu
6	835	86.0	411	S29129	calreticulin precu
7	804	82.8	405	JH0795	calreticulin precu
8	797	82.1	384	S29130	calreticulin (clon
9	796	82.0	419	S71343	calreticulin precu
10	699	72.0	406	A56637	calreticulin homol
11	619.5	63.8	395	S25851	calreticulin precu
12	542.5	55.9	336	A32507	41K larval antigen
13	539	55.5	412	T05703	calreticulin - bar
14	539	55.5	415	T05705	calreticulin - bar
15	536	55.2	421	S58170	calreticulin precu
16	531	54.7	416	T14554	calreticulin - bee
17	527	54.3	415	T10172	calreticulin - cas
18	522.5	53.8	421	S36799	calreticulin precu
19	522	53.8	416	T16988	calreticulin call
20	517	53.2	389	T03691	calreticulin - com
21	512	52.7	425	C96605	calreticulin (Crt1
22	510	52.5	444	T08624	hypothetical prote
23	496	51.1	393	A48573	calreticulin autoa
24	347	35.7	422	T07841	probable calreticu
25	293	30.2	591	T05434	calnexin precursor
26	290	29.9	591	T05434	calnexin precursor
27	290	29.9	592	T53260	calnexin - human
28	290	29.9	593	A37273	calnexin precursor
29	288	29.7	592	A46673	calnexin precursor

30	270	27.8	611	2	A53418	calnexin precursor
31	262	27.0	622	2	S71342	calnexin precursor
32	253.5	26.1	560	2	S56142	calcium-binding pr
33	252	26.0	611	2	A54066	calnexin-t - mouse
34	248	25.5	582	2	A46637	calnexin homolog S
35	244	25.1	619	2	S40938	calnexin-like prot
36	238.5	24.6	530	2	JN0597	calnexin-like prot
37	232	23.9	546	2	T06415	calnexin - soybean
38	215.5	22.2	540	2	T10892	probable calnexin
39	200.5	20.6	532	2	T49873	calnexin homolog -
40	157	16.2	29	2	E33208	calreticulin, uter
41	145	14.9	29	2	C33208	calreticulin, slow
42	144	14.8	29	2	D33208	calreticulin, brai
43	133.5	13.7	502	2	S29347	calnexin homolog Y
44	129	13.3	297	2	S70552	calnexin homolog C
45	124.5	12.8	428	2	T03251	calnexin - maize (

ALIGNMENTS

RESULT 1

A37047
calreticulin precursor - human
N:Alternate names: 52K ribonucleoprotein autoantigen Ro/SS-A; 60K integrin-binding prot;
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text change 09-Jul-2004
C:Accession: A42330; A37047; A46452; A28812; PH1525; A40346; S11475; T45075
R:McCaulliffe, D.P.; Yang, Y.S.; Wilson, J.; Sontheimer, R.D.; Capra, J.D.
J. Biol. Chem. 267, 2557-2562, 1992
A:Title: The 5'-flanking region of the human calreticulin gene shares homology with the
A:Reference number: A42330; MUID:92129342; PMID:1733953
A:Accession: A42330
A:Molecule type: DNA
A:Residues: 1-417 <MC2>
A:Cross-references: UNIPROT:P27797
A>Note: sequences extracted from NCBI backbone (NCBIN:78537, NCBIP:78536)
R:McCaulliffe, D.P.; Lux, F.A.; Lieu, T.S.; Sanz, I.; Hanke, J.; Newkirk, M.M.; Bachinski,
J. Clin. Invest. 85, 1379-1391, 1990
A:Title: Molecular cloning, expression, and chromosome 19 localization of a human Ro/SS
A:Reference number: A37047; MUID:90237213; PMID:2332496
A:Accession: A37047
A:Molecule type: mRNA
A:Residues: 1-417 <MCC>
A:Cross-references: GB:M32294; NID:G337486; PIDN:AAA36582.1; PID:G337487
R:Rocheach, L.A.; Haselby, J.A.; Meilof, J.F.; Smeenk, R.J.; Unnasch, T.R.; Greene, B.M.,
J. Immunol. 147, 3031-3039, 1991
A:Title: Characterization of the autoantigen calreticulin.
A:Reference number: A46452; MUID:92013129; PMID:1919005
A:Accession: A46452
A:Molecule type: mRNA
A:Residues: 1-417 <ROK>
A:Cross-references: GB:M84739; NID:G179881; PIDN:AAA51916.1; PID:G179882
A>Note: sequence extracted from NCBI backbone (RCBIN:60749, NCBIP:60750)
R:Lieu, T.S.; Newkirk, M.M.; Capra, J.D.; Sontheimer, R.D.
J. Clin. Invest. 82, 96-101, 1988
A:Title: Molecular characterization of human Ro/SS-A antigen. Amino terminal sequence o
A:Reference number: A28812; MUID:89273610; PMID:3260607
A:Accession: A28812
A:Molecule type: protein
A:Residues: 18-41 <LIE>
A>Note: 18-Ala was also found
R:Dupuis, M.; Schaefer, E.; Krause, K.H.; Tschopp, J.
J. Exp. Med. 177, 1-7, 1993
A:Title: The calcium-binding protein calreticulin is a major constituent of lytic granu
A:Reference number: PH1525; MUID:93115648; PMID:8418194
A:Accession: PH1525
A:Molecule type: protein
A:Residues: 18-27 <DUP>
A:Experimental source: LAK cell
R:Roijani, M.V.; Finlay, B.B.; Gray, V.; Dedhar, S.
Biochemistry 30, 9859-9866, 1991

A;Title: In vitro interaction of a polypeptide homologous to human Ro/SS-A antigen (calc
A;Reference number: A40346; MUID:92002034; PMID:1911778
A;Accession: A40346
A;Molecule type: protein
A;Residues: 18-34; <R>
R;Krause, K.H.; Simmerman, H.K.B.; Jones, L.R.; Campbell, K.P.
Biochem. J. 270, 545-548, 1990
A;Title: Sequence similarity of calreticulin with a Ca(2+)-binding protein that co-purif
A;Reference number: S11475; MUID:90380058; PMID:2400400
A;Accession: S11475
A;Molecule type: protein
A;Residues: 18-32 <R>
R;Ramerdin, J.; McCreedy, P.; Stilwagen, S.; Ramirez, M.; Carrano, A.
submitted to the EMBL Data Library, November 1996
A;Description: Characterization by genomic sequence analysis of a gene-rich 111 kb regio
A;Reference number: Z22906
A;Accession: T45075
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-417 <L>
A;Cross-references: EMBL:AD000092; PIDN:AAB51176.1
A;Experimental source: Cell line SH2-B; fibroblast
C;Comment: Autoantibodies specific for this protein are found in Sjogren's syndrome and
C;Genetics:
A;Gene: GDB:CALR
A;Cross-references: GDB:125179; OMIM:109091
A;Map position: 19p13.3-19p13.2
A;Intons: 31/1; 65/1; 133/1; 164/3; 234/3; 272/3; 320/3; 351/3
A;Note: CRT
C;Superfamily: calreticulin
C;Keywords: calcium binding; integrin binding
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F;18-417/Product: calreticulin #status predicted <MAT>
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Best Local Similarity 100.0%; Pred. No. 4.3e-81;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EBAVYFKEQFLDGDGWTSEWESKHSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
DB 18 EBAVYFKEQFLDGDGWTSEWESKHSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 77
QY 61 SASFPFNSKNGQTLVVOFTVKEQNIIDCGGVKFLPNSLQDTMHGDSSEYNIMFGPDIC 120
DB 78 SASFPFNSKNGQTLVVOFTVKEQNIIDCGGVKFLPNSLQDTMHGDSSEYNIMFGPDIC 137
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DB 138 GPGTKKHVHFNKGNVNLINKDIRKDBEFTHLYTLVPRDNTYEVKIDNSQVESGSL 197
RESULT 2
JH0819
calreticulin precursor - rat
N;Alternate names: calcium-binding protein 3
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence revision 20-Aug-1994 #text change 09-Jul-2004
C;Accession: JH0819; A49176; S11205; PC1109; S45036; S04867; S39372; A34473; S13045
R;Nakamura, M.; Moriya, M.; Baba, T.; Michikawa, Y.; Imanobe, T.; Arai, K.; Okinaga, S.
Exp. Cell Res. 205, 101-110, 1993
A;Title: An endoplasmic reticulum protein, calreticulin, is transported into the acrosom
A;Reference number: A49176; MUID:93202172; PMID:8453984
A;Accession: JH0819
A;Molecule type: mRNA
A;Residues: 1-416 <NA>
A;Cross-references: UNIPROT:P18418; GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g18455
A;Accession: A49176
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-416 <NA>
A;Cross-references: GB:D78308; NID:g1089798; PIDN:BA11345.1; PID:g1845572
A;Experimental source: Sprague-Dawley, spermatogenic cells

A;Note: sequence extracted from NCBI backbone (NCBIN:127639, NCBI:P127643)
R;Murthy, K.K.; Banville, D.; Srikant, C.B.; Carrier, F.; Holmes, C.; Bell, A.; Patel, Y.
Nucleic Acids Res. 18, 4933, 1990
A;Title: Structural homology between the rat calreticulin gene product and the Onchocerc
A;Reference number: S11205; MUID:90370496; PMID:2395661
A;Accession: S11205
A;Molecule type: mRNA
A;Residues: 1-416 <MUR>
A;Cross-references: EMBL:X53363; NID:G55854; PIDN:CAA37446.1; PID:G55855
R;Nakamura, M.; Michikawa, Y.; Baba, T.; Okinaga, S.; Arai, K.
Biochem. Biophys. Res. Commun. 186, 668-673, 1992
A;Title: Calreticulin is present in the acrosome of spermatozoa of rat testis.
A;Reference number: PC1109; MUID:92360010; PMID:1497655
A;Accession: PC1109
A;Molecule type: protein
A;Residues: 18-32 <NAK2>
A;Experimental source: testis, strain Sprague-Dawley
R;Sonnichsen, B.; Fuellekrug, J.; van Nguyen, P.; Diekmann, W.; Robinson, D.G.; Mieskes
submitted to the EMBL Data Library, May 1994
A;Description: Retention and retrieval: both mechanisms cooperate to maintain calreticul
A;Reference number: S45036
A;Accession: S45036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <SOE>
A;Cross-references: EMBL:X79327; NID:G488840; PIDN:CAAS5890.1; PID:G488841
R;Lone, Y.C.; Bailly, A.; Latruffe, N.
submitted to the EMBL Data Library, December 1988
A;Reference number: S04867
A;Accession: S04867
A;Molecule type: mRNA
A;Residues: 18-23, 'X', 25-32 <YOK>
A;Cross-references: EMBL:X13702; NID:G56055; PIDN:CAA31387.1; PID:G930260
A;Note: the authors designated the protein as D-beta-hydroxybutyrate dehydrogenase
R;Yokoi, T.; Nagayama, S.; Kajiura, R.; Kawaguchi, Y.; Horiuchi, R.; Kamataki, T.
Biochim. Biophys. Acta 1158, 339-344, 1993
A;Title: Identification of protein disulfide isomerase and calreticulin as autoimmune an
A;Reference number: S39371; MUID:94072621; PMID:8251535
A;Accession: S39372
A;Molecule type: protein
A;Residues: 18-23, 'X', 25-32 <YOK>
R;Van, P.N.; Peter, P.; Soeling, H.D.
J. Biol. Chem. 264, 17494-17501, 1989
A;Title: Four intracisternal calcium-binding glycoproteins from rat liver microsomes wit
itive calcium sequestering rat liver vesicles.
A;Reference number: A34473; MUID:90008920; PMID:2793869
A;Accession: A34473
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-36 <VAN>
R;Treves, S.; de Mattei, M.; Lanfredi, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A;Title: Calreticulin is a candidate for a calsequestrin-like function in Ca(2+)-storage
A;Reference number: S13045; MUID:91054414; PMID:2241926
A;Accession: S13045
A;Molecule type: protein
A;Residues: 18-29 <TRE>
C;Superfamily: calreticulin
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F;413-416/Region: endoplasmic reticulum retention #status predicted
F;344/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 96.1%; Score 933; DB 2; Length 416;
Best Local Similarity 94.4%; Pred. No. 1.3e-77;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 EBAVYFKEQFLDGDGWTSEWESKHSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
DB 18 DPAIFKQFLDGDGWTSEWESKHSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 77

QY 61 SASPEPNSKQTLVQVFTVKHEQNIIDCGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SARPEPNSKQTLVQVFTVKHEQNIIDCGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 137
QY 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSLE 197

RESULT 3
A34154
calreticulin precursor, skeletal muscle - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A34154; S13047
R:Pieleg, L.; Burns, K.; MacLennan, D.H.; Reithmeier, R.A.F.; Michalak, M.
J. Biol. Chem. 264, 21522-21528, 1989
A:Title: Molecular cloning of the high affinity calcium-binding protein (calreticulin) c
A:Reference number: A34154; MUID:900943320; PMID:2600080
A:Accession: A34154
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-418 <FLI>
A:Cross-references: UNIPROT:P15253; GB:J05138; NID:g164858; PIDN:AAA31188.1; PID:g164858
R:Treves, S.; de Mattei, M.; Lanfretti, M.; Villa, A.; Green, N.M.; MacLennan, D.H.; Meld
Biochem. J. 271, 473-480, 1990
A:Title: Calreticulin is a candidate for a calnexin-like function in Ca(2+)-storage
A:Reference number: S13045; MUID:91054414; PMID:2241926
A:Accession: S13047
A:Molecule type: protein
A:Residues: 19-32 <PRE>
C:Superfamily: calreticulin
C:Keywords: skeletal muscle
F:1-17/Domain: signal sequence #status predicted <SIG>
F:415-418/Region: endoplasmic reticulum retention signal

Query Match 95.9%; Score 931; DB 1; Length 418;
Best Local Similarity 95.6%; Pred. No. 1.9e-77; Indels 0; Gaps 0;
Matches 172; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
DB 18 EPVYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 77
QY 61 SASPEPNSKQTLVQVFTVKHEQNIIDCGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SARPEPNSKQTLVQVFTVKHEQNIIDCGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 137
QY 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSLE 197

RESULT 4
S43376
calreticulin, brain isoform 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Oct-1994 #sequence_revision 23-Mar-1995 #text_change 07-May-1999
C:Accession: S43376; S36801
R:Matsumoto, K.; Seta, K.; Yamakawa, Y.; Okuyama, T.; Shinoda, T.; Isobe, T.
Biochem. J. 299, 435-442, 1994
A:Title: Covalent structure of bovine brain calreticulin.
A:Reference number: S43376; MUID:94183174; PMID:8135753
A:Accession: S43376
A:Molecule type: protein
A:Residues: 1-400 <Mar>
A:Experimental source: brain
R:Liu, N.; Fine, R.E.; Johnson, R.J.
Biochim. Biophys. Acta 1202, 70-76, 1993
A:Title: Comparison of cDNAs from bovine brain coding for two isoforms of calreticulin.
A:Reference number: S36799; MUID:93385184; PMID:8373827
A:Accession: S36801
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 45-63, 'E', 65-83 <LIU>
A:Experimental source: brain, clone 8.1
C:Superfamily: calreticulin
C:Keywords: calcium binding; glycoprotein
F:397-400/Region: endoplasmic reticulum retention signal
F:120-146/Disulfide bonds: #status experimental
F:162/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 95.8%; Score 930; DB 2; Length 400;
Best Local Similarity 95.0%; Pred. No. 2.3e-77; Indels 0; Gaps 0;
Matches 171; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
DB 1 DPTVYFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
QY 61 SASPEPNSKQTLVQVFTVKHEQNIIDCGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 120
DB 61 SARPEPNSKQTLVQVFTVKHEQNIIDCGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 120
QY 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSLE 180
DB 121 GPGTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLVIRPNTYEVKIDNSQVSGSLE 180

RESULT 5
S06763
calreticulin precursor - mouse
N:Alternate names: 55K calcium-binding reticuloplasmin; calregulin
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S06763; JCI1444; FCI1233; A57498
R:Smith, M.J.; Koch, G.L.E.
EMBO J. 8, 3581-3586, 1989
A:Title: Multiple zones in the sequence of calreticulin (CRP55, calregulin, HACBP), a m
A:Reference number: S06763; MUID:90059955; PMID:2583110
A:Accession: S06763
A:Molecule type: DNA
A:Residues: 1-416 <SMI>
A:Cross-references: UNIPROT:P14211; EMBL:X14926; NID:g50567; PIDN:CAA33053.1; PID:g50567;
R:Marzarella, R.A.; Gold, P.; Cunningham, M.; Green, M.
Gene 120, 217-225, 1992
A:Title: Determination of the sequence of an expressible cDNA clone encoding Erp60/calr
A:Reference number: JCI1444; MUID:93013037; PMID:1398135
A:Accession: JCI1444
A:Molecule type: mRNA
A:Residues: 1-416 <MA2>
A:Cross-references: GB:M92988; NID:g193084; PIDN:AAA37569.1; PID:g193085
A:Accession: PC1233
A:Molecule type: protein
A:Residues: 18-41 <MA2>
R:White, T.K.; Zhu, Q.; Tanzer, M.L.
J. Biol. Chem. 270, 15926-15929, 1995
A:Title: Cell surface calreticulin is a putative mannose lectin which triggers mouse
A:Reference number: A57498; MUID:95332280; PMID:7608143
A:Accession: A57498
A:Status: preliminary
A:Molecule type: protein
A:Residues: 74-80; 142-151; 186-193 <WHI>
C:Superfamily: calreticulin
C:Keywords: calcium binding
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-416/Product: calregulin #status experimental <MAT>
F:413-416/Region: endoplasmic reticulum retention signal

Query Match 95.8%; Score 930; DB 1; Length 416;
Best Local Similarity 94.4%; Pred. No. 2.4e-77; Indels 0; Gaps 0;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
DB 18 DPALVFKQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 77

QY 61 SASPEPSNKGQTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDIC 120
 Db 78 SAKFPEPSNKGQTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDIC 137

QY 121 GPQTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSQVSGSLE 180
 Db 138 GPQTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSQVSGSLE 197

RESULT 6

S29129
 calreticulin precursor (clone 3) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: S29129
 R:Trevies, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992
 A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218

A:Accession: S29129
 A:Molecule type: mRNA
 A:Residues: 1-411 <TR>
 A:Cross-references: UNIPROT:Q91710; EMBL:X67597; NID:G64608; PIDN:CAA47866.1; PID:G64609
 C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>
 F:13-411/Product: calreticulin #status predicted <MAT>
 F:408-411/Region: endoplasmic reticulum retention signal
 F:339/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 86.0%; Score 835; DB 2; Length 411;
 Best Local Similarity 83.9%; Pred. No. 1.1e-68;
 Matches 151; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSMWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60
 Db 13 EPAVYFKEFTDGDGWTQWRWESKHKIDGKFLSAGKFGYDSEKDKGLQTSQDARFYAM 72

QY 61 SASPEPSNKGQTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDIC 120
 Db 73 SSRFDSFNKQDQTLVQVQSKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDIC 132

QY 121 GPQTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSQVSGSLE 180
 Db 133 GPPTKKVHVIFQYKKNIQINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSKVSLE 192

RESULT 7

JH0795
 calreticulin precursor - California sea hare
 N:Alternate names: protein 407
 C:Species: Aplysia californica (California sea hare)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0795; B31409; F60977
 R:Kennedy, T.E.; Kuhl, D.; Barzilai, A.; Sweatt, J.D.; Kandel, E.R.
 Neuron 9, 1013-1024, 1992
 A:Title: Long-term sensitization training in aplysia leads to an increase in calreticulin
 A:Reference number: JH0795; MUID:93098937; PMID:1463604

A:Accession: JH0795
 A:Molecule type: mRNA
 A:Residues: 1-405 <XEN>
 A:Cross-references: GB:S51239; NID:Q262053; PIDN:AA24569.1; PID:G262054
 A:Experimental source: abdominal ganglion and antral nervous system
 R:Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, E.R.; Sweatt, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 89, 7008-7012, 1992
 A:Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and
 tion in Aplysia.

A:Reference number: A94207; MUID:86320566; PMID:3413132
 A:Accession: B31409
 A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <KE2>
 R:Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K.

Electrophoresis 10, 152-157, 1989

A:Title: Development of a database of amino acid sequences for proteins identified and i
 A:Reference number: A60977; MUID:89276264; PMID:2731514
 A:Accession: F60977

A:Molecule type: protein
 A:Residues: 'X', 17-28, 'X', 30-31 <SWE>
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:16-405/Product: calreticulin #status experimental <MAT>
 F:402-405/Region: endoplasmic reticulum retention signal

Query Match 82.8%; Score 804; DB 1; Length 405;

Best Local Similarity 79.4%; Pred. No. 7.7e-66;
 Matches 143; Conservative 18; Mismatches 17; Indels 2; Gaps 1;

QY 1 EPAVYFKEQFLDGDGWTSMWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYAL 60

Db 16 DPTVYFKEEF--GDDWAERWVESKHKSGLCKPVLTAGKFYDGAEDKDKGLQTSQDARFYGL 73

QY 61 SASPEPSNKGQTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDIC 120

Db 74 SAKFPEPSNKGQTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDIC 133

QY 121 GPQTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSQVSGSLE 180

Db 134 GPQTKKVHVIFNYKGNVNLINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNEKESGSDLE 193

RESULT 8

S29130
 calreticulin (clone 8) - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: S29130; T01068
 R:Trevies, S.; Zorzato, F.; Pozzan, T.
 Biochem. J. 287, 579-581, 1992

A:Title: Identification of calreticulin isoforms in the central nervous system.
 A:Reference number: S29129; MUID:93074997; PMID:1445218
 A:Accession: S29130
 A:Molecule type: mRNA

A:Residues: 1-384 <TR>
 A:Cross-references: UNIPROT:Q91711; EMBL:X67598
 A:Accession: T01068
 A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-339, 'X' <TR>
 A:Cross-references: EMBL:X67598; NID:G64610; PIDN:CAA47867.1; PID:G64611
 A:Experimental source: CNS

C:Superfamily: calreticulin
 C:Keywords: glycoprotein
 F:381-384/Region: endoplasmic reticulum retention signal
 F:316/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.1%; Score 797; DB 2; Length 384;

Best Local Similarity 85.2%; Pred. No. 3.1e-65;
 Matches 144; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 12 DGDGWTSMWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFYALSASFEPFNKG 71

Db 1 DGDGWTQWRWESKHKSDFGKFLSAGKFGYDSEKDKGLQTSQDARFYAMSSRFESFNKD 60

QY 72 QTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDICGGPTKKVHVIF 131

Db 61 QTLVQVQTKHEQNDICGGYVVKLFPSNLDQTDMDHGDSEYNIIMFGPDICGGPTKKVHVIF 120

QY 132 NYKGNVNLINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSQVSGSLE 180

Db 121 QYKKNLQINKIRCKDDEFTHTLYTLIVRPNTVEVKIDNSQVSGSLE 169

RESULT 9

S71343

calreticulin precursor - Korean frog
 C:Species: Rana rugosa (Korean frog)
 C>Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000
 C:Accession: S71343
 R:Yamamoto, S.; Nakamura, M.
 FEBS Lett. 387, 27-32, 1996
 A>Title: Calnexin: its molecular cloning and expression in the liver of the frog, Rana rugosa
 A:Reference number: S71342; MUID:96234004; PMID:8654561
 A:Accession: S71343
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-419 <YAN>
 A:Cross-references: EMBL:D78589; NID:G1514956; PIDN:BAAL1425.1; PID:G1514957
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-18/Domain: signal sequence #status predicted <SIG>
 F:19-419/Product: calreticulin #status predicted <MAT>
 F:205-213/Region: nuclear location signal
 F:415-418/Region: endoplasmic reticulum retention signal

Query Match 82.0%; Score 796; DB 2; Length 419;
 Best Local Similarity 80.6%; Pred. No. 4.3e-65;
 Matches 145; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

QY 1 BPVYKQFLDGGWTSRWIESKHK-SDFGKFLVLSGKFGYDEEKDGLQTSQDARFYALSA 60
 DB 19 KPAVTFQEGFDGDAWNERIQSKHSDYIGQFKLSAGKFGDEEKDGLQTSQDARFYAH 78

QY 61 SASFEPFNKQGLVQVFTVKEHQINIDCGGGYVKLFPSNLDQTDMDHGDSEYNIMFGPDIC 120
 DB 79 SAGFPAPFNKQGLVQVFTVKEHQINIDCGGGYVKLFPSNLDQTDMDHGDSEYNIMFGPDIC 138

QY 121 GPGTKKHVIFNYKGNVILNKDIRCKDDFTHLYTLVLRPNTYEVKIDNSQVSGSLE 180
 DB 139 GPPTKHVIFNYKGNVILNKDIRCKDDFTHLYTLVLRPNTYEVKIDNSQVSGSLE 198

RESULT 10
 A56637
 A>Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
 A:Alternate names: Ro/SS-A autoantigen/calreticulin homolog
 C:Species: Drosophila melanogaster
 C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
 C:Accession: A56637; A37158
 R:Smith, M.J.
 DNA Seq. 3, 247-250, 1992
 A>Title: Nucleotide sequence of a Drosophila melanogaster gene encoding a calreticulin homolog precursor - fruit fly (Drosophila melanogaster)
 A:Reference number: A56637; MUID:93208374; PMID:1236819
 A:Accession: A56637
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-406 <SMI>
 A:Cross-references: UNIPROT:P29413; GB:X64461; NID:G7685; PIDN:CAA45791.1; PID:G7686
 A>Note: sequence extracted from NCBI backbone (NCBIN:128274, NCBIIP:128275)
 R:McCaulliffe, D.P.; Zappi, E.; Lieu, T.S.; Michalak, M.; Sontheimer, R.D.; Capra, J.D.
 J. Clin. Invest. 96, 332-335, 1990
 A>Title: A human Ro/SS-A autoantigen is the homologue of calreticulin and is highly homologous to the Drosophila melanogaster Ro/SS-A autoantigen
 A:Reference number: A37158; MUID:90307981; PMID:1236582
 A:Accession: A37158
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 91-105, 'A', 107, 109-124, 182-183, 'L', 185-220 <MCC>
 C:Genetics:
 A:Gene: FlyBase:Crc
 A:Cross-references: FlyBase:FBgn0005585
 A:Introns: 65/1; 222/3
 C:Superfamily: calreticulin
 C:Keywords: calcium binding; endoplasmic reticulum
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:403-406/Region: endoplasmic reticulum retention signal

Query Match 72.0%; Score 699; DB 2; Length 406;
 Best Local Similarity 74.2%; Pred. No. 3.1e-56;

Matches 132; Conservative 14; Mismatches 30; Indels 2; Gaps 2;
 QY 4 VYFKEQFLDGGWTSRWIESKHK-SDFGKFLVLSGKFGYDEEKDGLQTSQDARFYALSA 62
 DB 21 VYLKENF-DNENWEDTWYKSGKFGKFLVLPSTPGTFYNDAAEADKGIQTSQDARFYAASR 79

QY 63 SFEPFNKQGLVQVFTVKEHQINIDCGGGYVKLFPSNLDQTDMDHGDSEYNIMFGPDICGP 122
 DB 80 KFDGFSNEDKPLVQVFTVKEHQINIDCGGGYVKLFPSNLDQTDMDHGDSEYNIMFGPDICGP 139

QY 123 GPKKHVIFNYKGNVILNKDIRCKDDFTHLYTLVLRPNTYEVKIDNSQVSGSLE 180
 DB 140 GPKKHVIFNYKGNVILNKDIRCKDDFTHLYTLVLRPNTYEVKIDNSQVSGSLE 197

RESULT 11
 S25851
 A>Title: calreticulin precursor - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 06-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S25851; T33996
 R:Smith, M.J.
 DNA Seq. 2, 235-240, 1992
 A>Title: A C. elegans gene encodes a protein homologous to mammalian calreticulin.
 A:Reference number: S25851; MUID:92329975; PMID:1627827
 A:Accession: S25851
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-395 <SMI>
 A:Cross-references: UNIPROT:P27798; EMBL:X59589; NID:G6693; PIDN:CAA42159.1; PID:G6694
 R:Bauer, C.; Courtney, L.; Lapiant, Y.
 Submitted to the EMBL Data Library, February 1999
 A>Description: The sequence of C. elegans cosmid Y38A10A.
 A:Reference number: Z21453
 A:Accession: T33996
 A>Status: preliminary; translated from GE/EMBL/DDSV
 A:Molecule type: DNA
 A:Residues: 1-395 <BAU>
 A:Cross-references: EMBL:AF125963; PIDN:AADI4746.1; GSPDB:GNO0023; CESP:Y38A10A.5
 A:Experimental source: strain Bristol N2; clone Y38A10A
 C:Genetics:
 A:Gene: CESP:Y38A10A.5
 A:Map position: 5
 A:Introns: 107/3; 315/3
 C:Superfamily: calreticulin
 F:1-15/Domain: signal sequence #status predicted <SIG>
 F:392-395/Region: endoplasmic reticulum retention signal

Query Match 63.8%; Score 619.5; DB 2; Length 395;
 Best Local Similarity 63.5%; Pred. No. 5.5e-49;
 Matches 113; Conservative 26; Mismatches 36; Indels 3; Gaps 3;

QY 4 VYFKEQFLDGGWTSRWIESKHKSDFGKFLVLSGKFGYDEEKDGLQTSQDARFYALSA 63
 DB 17 VYFKEFNDA-SWEKRWVQSKHKKDDFGAFKLSAGKFGDEESRDQGIQTSQDAKFYSRAAK 75

QY 64 FE-PFSNKGQTLVQVFTVKEHQINIDCGGGYVKLFPSNLDQTDMDHGDSEYNIMFGPDICGP 122
 DB 76 FDKDFSNKGQTLVQVFTVKEHQINIDCGGGYVKLVWRADADLGDGFGHGETPYNVIMFGPDICGP 135

QY 123 GPKKHVIFNYKGNVILNKDIRCKDDFTHLYTLVLRPNTYEVKIDNSQVSGSLE 180
 DB 136 TRRVHVLNKGKGLIKKEITCKSDDELTHLYTLILNSDNTYEVKIDGESAQTSLE 192

RESULT 12
 A32507
 A>Title: 41K larval antigen - nematode (Onchocerca volvulus) (fragment)
 C:Species: Onchocerca volvulus
 C>Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
 C:Accession: A32507; A28813
 R:Junnasch, T.R.; Gallin, M.Y.; Soboslay, P.T.; Erttmann, K.D.; Greene, B.M.
 J. Clin. Invest. 82, 262-269, 1988

A:Title: Isolation and characterization of expression cDNA clones encoding antigens of calreticulin - barley (fragment)
 A:Reference number: A92769; MUID:88273584; PMID:2455736
 A:Accession: T05703

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-336 <UN>

A:Cross-references: UNIPROT:P11012

C:Superfamily: calreticulin

Query Match 55.9%; Score 542.5; DB 2; Length 336;
 Best Local Similarity 68.5%; Pred. No. 4.9e-42;
 Matches 98; Conservative 22; Mismatches 22; Indels 1; Gaps 1;

QY 39 FYGDEKDKGLQTSQDAFYALSASPE-PFSNKGQTLVQFTVHEQNDICGGVYKLP 97

Db 1 FYGDAVKDKGLTKTQDAKFSYIGAKFDKFSNKGSLVTFQSVKHEQDIDCGGVYKLA 60

QY 98 NSLDQTMHGDSEYINMFGPDICGPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHLYTL 157

Db 61 SDVNLEDHGETPHIMFGPDICGPGTKKVVHVFNYKGNVLIINKDIRCKDDVFTHLYTL 120

QY 158 IVPNDTYEVKIDNSOVESGSL 180

Db 121 IVNSDNTYEVQIDGERAESGELE 143

RESULT 13

T05703

calreticulin - barley (fragment)

C:Species: Hordeum vulgare (barley)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05703

R:Chen, F.; Hayes, P.M.; Mulroony, D.; Pan, A.

Plant Cell 6, 835-843, 1994

A:Title: Identification and characterization of cDNA clones encoding plant calreticulin

A:Reference number: Z15422; MUID:94339696; PMID:7914763

A:Accession: T05703

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-412 <CHE>

A:Cross-references: UNIPROT:Q40040; EMBL:L27348; NID:G439585; PIDN:AAA32948.1; PID:G4395

A:Experimental source: cv. Morex, ovary

C:Genetics:

A:Gene: CRH1

A:Map position: 1M

C:Superfamily: calreticulin

C:Keywords: calcium binding

Query Match 55.5%; Score 539; DB 2; Length 412;
 Best Local Similarity 56.4%; Pred. No. 1.3e-41;
 Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSRWIESKHSD---FGKVLSSGKFYGDDEKDKGLQTSQDAFYAL 60

Db 20 VFFQKEF--EDGWESRWKSEWKKDENMAGWNHTSGKWHGDAE-DKGIQTSQDAFYAL 76

QY 61 SASPEPFSNKGQTLVQFTVHEQNDICGGVYKLPNSLDQTMHGDSEYINMFGPDIC 120

Db 77 SAYPEPFSNKGQTLVQFTVHEQNDICGGVYKLPNSLDQTMHGDSEYINMFGPDIC 136

QY 121 GPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSOVESGSL 179

Db 137 GYSTKKVHTLTNKGKNNHLIKDVPCTDQLSHVYTLIRPDATYSILIDNEEKQTGSI 195

RESULT 14

T05705

calreticulin - barley (fragment)

C:Species: Hordeum vulgare (barley)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05705

R:Chen, F.; Hayes, P.M.; Mulroony, D.; Pan, A.

Plant Cell 6, 835-843, 1994

A:Title: Identification and characterization of cDNA clones encoding plant calreticulin

A:Reference number: Z15422; MUID:94339696; PMID:7914763

A:Accession: T05705

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-415 <CHE>

A:Cross-references: UNIPROT:Q40041; EMBL:L27349; NID:G439587; PIDN:AAA32949.1; PID:G4395

A:Experimental source: cv. Morex, ovary

C:Genetics:

A:Gene: CRH2

A:Map position: 2M

C:Superfamily: calreticulin

C:Keywords: calcium binding

Query Match 55.5%; Score 539; DB 2; Length 415;
 Best Local Similarity 56.4%; Pred. No. 1.3e-41;
 Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSRWIESKHSD---FGKVLSSGKFYGDDEKDKGLQTSQDAFYAL 60

Db 23 VFFQKEF--EDGWESRWKSEWKKDENMAGWNHTSGKWHGDAE-DKGIQTSQDAFYAL 79

QY 61 SASPEPFSNKGQTLVQFTVHEQNDICGGVYKLPNSLDQTMHGDSEYINMFGPDIC 120

Db 80 SAYPEPFSNKGQTLVQFTVHEQNDICGGVYKLPNSLDQTMHGDSEYINMFGPDIC 139

QY 121 GPGTKKVVHVFNYKGNVLIINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSOVESGSL 179

Db 140 GYSTKKVHTLTNKGKNNHLIKDVPCTDQLSHVYTLIRPDATYSILIDNEEKQTGSI 198

RESULT 15

S58170

calreticulin precursor - maize

C:Species: Zea mays (maize)

C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 13-Aug-1999

C:Accession: S58170; S49818

R:Dresselhaus, T.; Hagel, C.; Loerz, H.; Kranz, E.

submitted to the EMBL Data Library, July 1995

A:Description: Isolation of a cDNA encoding Calreticulin from in vitro zygotes of maize.

A:Reference number: S58170

A:Accession: S58170

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-421 <DRE>

A:Cross-references: EMBL:X89813; NID:G927571; PIDN:CAA61939.1; PID:G927572

R:Napier, R.M.; Trueman, S.; Henderson, J.; Boyce, J.M.; Hawes, C.R.; Ficker, M.D.; Ven

submitted to the EMBL Data Library, November 1994

A:Description: Purification and sequencing of calreticulin from maize and evidence for it

A:Reference number: S49818

A:Accession: S49818

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-421 <NAP>

A:Cross-references: EMBL:Z46772; NID:G577611; PIDN:CAA86728.1; PID:G577612

C:Genetics:

A:Gene: CRT1

C:Superfamily: calreticulin

C:Keywords: calcium binding

F:1-25/Domain: signal sequence #status predicted <SIG>

F:418-421/Region: endoplasmic reticulum retention signal

Query Match 55.2%; Score 536; DB 2; Length 421;
 Best Local Similarity 56.4%; Pred. No. 2.6e-41;
 Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY 4 VYFKEQFLDGDGWTSRWIESKHSD---FGKVLSSGKFYGDDEKDKGLQTSQDAFYAL 60

Db 27 VFFQKEF--EDGWESRWKSEWKKDENMAGWNHTSGKWHGDAE-DKGIQTSQDAFYAL 83

QY 61 SASPEPFSNKGQTLVQFTVHEQNDICGGVYKLPNSLDQTMHGDSEYINMFGPDIC 120

Db 84 SAYPEPFSNKGQTLVQFTVHEQNDICGGVYKLPNSLDQTMHGDSEYINMFGPDIC 143

Oy 121 GPGTKKVHVFNYKGNVLINKDIRCKDDEFTHLYTLIVRPNTYEVKIDNSQVESGSL 179
Db 144 GYSTKKVHTLTCKDGNHLIKDVFCTDQLTHVYTLIIRPDATYSILIDNEEKQTGSI 202

Search completed: October 15, 2004, 13:12:53
Job time : 15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2004, 13:11:18 ; Search time 155 Seconds

(without alignments)
416.589 Million cell updates/sec

Title: US-09-807-148-4

Perfect score: 971

Sequence: 1 EPAYVFKQFLDGDGWTSRW.....PDNTVEVKIDNSQVSGSLE 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_23sep04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001s:*
 - 5: Geneseq2002s:*
 - 6: Geneseq2003as:*
 - 7: Geneseq2003bs:*
 - 8: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	971	100.0	180	3	AAY92351 Human vas
2	971	100.0	387	7	ADG75706 Human pro
3	971	100.0	400	3	AAY92350 Recombina
4	971	100.0	417	1	AAP92276 60 KD RO
5	971	100.0	417	3	AAY92349 Human MBP
6	971	100.0	417	5	AAY77712 Human cal
7	971	100.0	417	5	AAY24591 Human cal
8	971	100.0	417	5	AAE18851 Human cal
9	971	100.0	417	5	ABJ19766 Human cal
10	971	100.0	417	6	ABJ19766 Human cal
11	971	100.0	417	6	ADA79824 Calreticu
12	971	100.0	417	6	ADA79824 Human cal
13	971	100.0	417	7	ADD22407 HLA-B46 T
14	971	100.0	417	7	ADG56308 Human Pro
15	971	100.0	417	7	ADG56312 Human Pro
16	971	100.0	417	7	ADG56312 Human Pro
17	971	100.0	417	7	ADG56312 Human Pro
18	971	100.0	417	8	ADN03688 Antipeptid
19	966	99.5	417	8	ADO19114 Human PRO
20	933	96.1	416	7	AAY00927 Calreticu
21	933	96.1	416	7	ADG56306 Rat Prote
22	933	96.1	416	7	ADG56310 Rat Prote
23	933	96.1	416	7	ADG56310 Rat Prote
24	933	96.1	416	7	ADG56310 Rat Prote
25	921	94.9	401	2	AAW11156 Calreticu

26	700	72.1	403	2	AAW04171 Flea calr
27	699	72.0	406	4	ABG4414 Drosophil
28	631	65.0	384	7	AD157351 Human cal
29	631	65.0	385	3	AAB32385 Human sec
30	631	65.0	390	6	ABO07134 Novel hum
31	616.5	63.5	177	5	ABP42414 Human ova
32	541.5	55.8	336	2	AAR12312 Partial s
33	540	55.6	419	7	ABM74155 DNA clone
34	527	54.3	415	4	AAB66343 Castor be
35	527	54.3	415	4	AAB66341 Castor be
36	510	52.5	421	3	AG24608 Arabidops
37	510	52.5	421	3	AG24607 Arabidops
38	510	52.5	424	3	AG24607 Arabidops
39	510	52.5	441	3	AG30997 Arabidops
40	510	52.5	444	3	AG30996 Arabidops
41	494	50.9	420	5	ABM04656 Maize cal
42	486	50.1	428	7	ABM74288 DNA clone
43	327	33.7	61	3	AY92352 Recombina
44	318	32.7	60	3	AY92354 Recombina
45					

ALIGNMENTS

RESULT 1

AY92351

ID AAY92351 standard; protein; 180 AA.

XX

AC AAY92351;

XX

DT 10-AUG-2000 (first entry)

XX

DE Human vasostatin (calreticulin N-terminal 180 amino acids).

XX

KW MBP-calreticulin; maltose binding protein; vasostatin; N-terminal; angiogenesis; inhibition; endothelial cell; anti-angiogenic; neuroprotective; antidiabetic; cytostatic; dermatological; hepatic; immunosuppressive; antiinflammatory; anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.

XX

OS Homo sapiens.

OS Synthetic.

XX

FN WO200020577-A1.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-US023240.

XX

PR 06-OCT-1998; 98US-0103438P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Tosato G, Pike SE, Yao L;

XX

WPI; 2000-303767/26.

XX

PT Inhibiting endothelial cell growth and angiogenesis using calreticulin, useful for suppressing tumor growth.

XX

PS Claim 4; Page 82; 99pp; English.

XX

CC A novel method of inhibiting endothelial cell growth comprises contacting the cells with calreticulin (or its fragments/variants). Fragments of calreticulin causes at least 40% inhibition of angiogenesis, tumor growth and/or endothelial cell growth (claimed). The method may be used for inhibiting angiogenesis in a patient. The angiogenesis is associated with a disease other than a tumor that is associated with neovascularization (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular glaucoma, psoriasis, angiodiomas, immune inflammation, atherosclerosis, excessive wound repair, retinal neovascularization, macular degeneration, corneal graft rejection, contact lens overwear,

CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX Sequence 180 AA;
 SQ

Query Match 100.0%; Score 971; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred No. 4.4e-99;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVLSGKFGYDDEKDKGLQTSQDARFYAL 60
 Db 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVLSGKFGYDDEKDKGLQTSQDARFYAL 60

QY 61 SASFEFPSNKGOTLVVQFTVKHEQNIIDCGGVVVKLFPSLSDOTDMHGDSEYNIMFGPDIC 120
 Db 61 SASFEFPSNKGOTLVVQFTVKHEQNIIDCGGVVVKLFPSLSDOTDMHGDSEYNIMFGPDIC 120

QY 121 GPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 Db 121 GPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180

RESULT 2
 ADG75706
 ID ADG75706 standard; protein; 387 AA.
 AC ADG75706;
 XX
 DT 11-MAR-2004 (first entry)
 DE Human protein modification and maintenance molecule polypeptide SeqID30.
 XX human; protein modification and maintenance molecule; PMMW; kinase;
 KW phosphatase; protease; protease inhibitor; isomerase; transferase;
 KW molecular chaperone; gastrointestinal; cardiovascular; autoimmune;
 KW inflammatory; cell proliferative; developmental; epithelial;
 KW neurological; reproductive disorder; enzyme;
 KW single nucleotide polymorphism; SNP.
 XX
 OS Homo sapiens.
 XX
 PN WO2003083084-A2.
 XX
 PD 09-OCT-2003.
 XX
 PF 26-MAR-2003; 2003WO-US009774.
 XX
 PR 29-MAR-2002; 2002US-0368686P.
 PR 03-MAY-2002; 2002US-0377489P.
 PR 03-MAY-2002; 2002US-0378205P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Lal PG, Tang YT, Lee SY, Griffin JA, Elliott VS, Khare R;
 PI Ramkumar J, Richardson TW, Ison CH, Hafalia AJA, Kable AE;
 PI Swarnakar A, Chang H, Bhatia US, Burrill JD, Lee S, Blake JJ, Ho A;
 PI Zheng W, Chawla NK, Marquis JP, Tran UK, Emerling EK, Mason PM;
 PI Becha SD, Warren BA, Au-Young JK, Lee EA, Gietzen KU, Jiang X;
 PI Jackson AA, Baughn MR, Wilson AD, Jin P, Bulloch SA;
 XX
 DR WPI; 2003-812541/76.
 DR N-PSDB; ADG75776.
 XX
 PT New human protein modification and maintenance molecules (PMMW)
 PT polypeptide, useful for preparing a composition for treating a disease
 PT associated with decreased expression or overexpression of PMMW e.g.,
 PT cancer.
 XX
 PS Claim 1; SEQ ID NO 30; 500pp; English.
 PS
 XX

CC This invention relates to novel isolated polynucleotides that encode
 CC human protein modification and maintenance molecules (PMMW).
 CC Specifically, it refers to key enzymes and proteins such as kinases,
 CC phosphatases, proteases, protease inhibitors, isomerases, transferases
 CC and molecular chaperones that modify and maintain protein molecules by co-
 CC-ordinating their function, conformation, stabilisation and degradation.
 CC The present invention describes antibodies, agonists and antagonists (as
 CC well as single nucleotide polymorphisms) that can be useful for the
 CC diagnosis, treatment and prevention of disorders associated with the
 CC aberrant expression of PMMW, which includes gastrointestinal,
 CC cardiovascular, autoimmune/ inflammatory, cell proliferative,
 CC developmental, epithelial, neurological and reproductive disorders.
 CC Furthermore, the invention relates to the effect of exogenous compounds
 CC on the expression of PMMWs. This polypeptide is a human PMMW protein of
 CC the invention.

SQ Sequence 387 AA;

Query Match 100.0%; Score 971; DB 7; Length 387;
 Best Local Similarity 100.0%; Pred No. 1.3e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVLSGKFGYDDEKDKGLQTSQDARFYAL 60
 Db 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVLSGKFGYDDEKDKGLQTSQDARFYAL 77

QY 61 SASFEFPSNKGOTLVVQFTVKHEQNIIDCGGVVVKLFPSLSDOTDMHGDSEYNIMFGPDIC 120
 Db 78 SASFEFPSNKGOTLVVQFTVKHEQNIIDCGGVVVKLFPSLSDOTDMHGDSEYNIMFGPDIC 137

QY 121 GPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 Db 138 GPCTKKVHVFYFNKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 3
 AAY92350
 ID AAY92350 standard; protein; 400 AA.
 XX
 AC AAY92350;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Recombinant human MBP-calreticulin.
 XX
 KW MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
 KW endothelial cell; anti-angiogenic; neuroprotective; antidiabetic;
 KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
 KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
 XX
 OS Homo sapiens.
 XX
 PN WO200020577-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 05-OCT-1999; 99WO-US023240.
 XX
 PR 06-OCT-1998; 98US-0103438P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Tosato G, Pike SE, Yao L;
 XX
 DR WPI; 2000-303767/26.
 DR N-PSDB; AAA09346, AAA09347.
 XX
 PT Inhibiting endothelial cell growth and angiogenesis using calreticulin,
 PT useful for suppressing tumor growth.
 XX
 PS Claim 4; Page 80-81; 99pp; English.
 PS
 XX Recombinant human MBP-calreticulin comprises the sequence of human

CC autoimmunity diseases. These epitopes are AAs 24-36, 23-36, 188-209, or 241
CC -255. The peptides may be substd. for ribonucleoprotein particle
CC antigens. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC MAR-2003 to correct PI field.)
XX
SQ Sequence 417 AA;
Query Match 100.0%; Score 971; DB 1; Length 417;
Best Local Similarity 100.0%; Pred. NO. 1.4e-98;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EPAYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGVDEEKDKGLQTSQDARFYAL 60
Db 18 EPAYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGVDEEKDKGLQTSQDARFYAL 77
Qy 61 SASFEFNSKQTLVQVTVKHEQNIIDCGGYYVLPNSLDQTDMDHGDSEYNIMFGPDIC 120
Db 78 SASFEFNSKQTLVQVTVKHEQNIIDCGGYYVLPNSLDQTDMDHGDSEYNIMFGPDIC 137
Qy 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSLE 180
Db 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSLE 197
RESULT 5
ID AAY92349 standard; protein; 417 AA.
XX AAY92349;
AC AAY92349;
XX 10-AUG-2000 (first entry)
DT Human MBP-calreticulin.
DE MBP-calreticulin; maltose binding protein; angiogenesis; inhibition;
XX endotheial cell; anti-angiogenic; neuroprotective; antidiabetic;
KW cytostatic; dermalogical; immunosuppressive; antiinflammatory; hepatic;
KW anti-atherosclerotic; gastrointestinal; anti-arthritis; ophthalmic.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1. 17
FT /label= signal_peptide
FT Protein 18
FT /label= mature_protein
XX WO200020577-A1.
PN 13-APR-2000.
XX
XX 05-OCT-1999; 99WO-US023240.
PF
XX 06-OCT-1998; 98US-0103438P.
PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Tosato G, Pike SE, Yao L;
PI WPI, 2000-303767/26.
XX N-PSDB; AAA09346, AAA09347.
DR
XX Inhibiting endothelial cell growth and angiogenesis using calreticulin,
PT useful for suppressing tumor growth.
XX
XX Disclosure; Page 79-80; 99pp; English.
XX A novel method of inhibiting endothelial cell growth comprises contacting
CC the cells with calreticulin (or its fragments/variants). Fragments of
CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
CC and/or endothelial cell growth (claimed). The method may be used for
CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
CC a disease other than a tumor that is associated with neovascularization
CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
CC glaucoma, psoriasis, angiodermas, immune inflammation,
CC atherosclerosis, excessive wound repair, retinal neovascularization,
CC macular degeneration, corneal graft rejection, contact lens overwear,
CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
CC biliary cirrhosis). The method may also be used for treating/inhibiting
CC tumor growth especially Kaposi's sarcoma (claimed)
XX
SQ Sequence 400 AA;
Query Match 100.0%; Score 971; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. NO. 1.3e-98;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EPAYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGVDEEKDKGLQTSQDARFYAL 60
Db 1 EPAYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGVDEEKDKGLQTSQDARFYAL 60
Qy 61 SASFEFNSKQTLVQVTVKHEQNIIDCGGYYVLPNSLDQTDMDHGDSEYNIMFGPDIC 120
Db 61 SASFEFNSKQTLVQVTVKHEQNIIDCGGYYVLPNSLDQTDMDHGDSEYNIMFGPDIC 120
Qy 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSLE 180
Db 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSLE 180
RESULT 4
ID AAP92276 standard; protein; 417 AA.
XX AAP92276;
AC AAP92276;
XX 25-MAR-2003 (revised)
DT 23-FEB-1990 (first entry)
XX 60 kD Ro (Rc/SSA) antigen.
DE
XX Sjorens syndrome; systemic lupus erythematosus.
KW
XX Synthetic.
CS
XX WO8909273-A.
PN
XX 05-OCT-1989.
PD
XX 22-MAR-1989; 89WO-US001213.
PF
XX 22-MAR-1988; 88US-00171634.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX Sontheimer RD, Lieu TS, Capra JD, Mccaulliffe DP;
PI WPI; 1989-309537/42.
XX N-PSDB; AAP92276.
DR
XX DNA sequences encoding antigenic epitope(s) of Ro 60 auto-antigen -
PT used in immunoassays to detect rheumatic disease.
PT
XX Disclosure; Fig 2; 88pp; English.
PS
XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification of
CC

CC calreticulin (see AAY92349) without the 17 N-terminal amino acids. A
CC novel method of inhibiting endothelial cell growth comprises contacting
CC the cells with calreticulin (or its fragments/variants). Fragments of
CC calreticulin causes at least 40% inhibition of angiogenesis, tumor growth
CC and/or endothelial cell growth (claimed). The method may be used for
CC inhibiting angiogenesis in a patient. The angiogenesis is associated with
CC a disease other than a tumor that is associated with neovascularization
CC (e.g. diabetic neuropathy, retrolental fibroplasia, trachoma, neovascular
CC glaucoma, psoriasis, angiodermas, immune inflammation,
CC atherosclerosis, excessive wound repair, retinal neovascularization,
CC macular degeneration, corneal graft rejection, contact lens overwear,
CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
CC biliary cirrhosis). The method may also be used for treating/inhibiting
CC tumor growth especially Kaposi's sarcoma (claimed)
XX
SQ Sequence 400 AA;
Query Match 100.0%; Score 971; DB 3; Length 400;
Best Local Similarity 100.0%; Pred. NO. 1.3e-98;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EPAYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGVDEEKDKGLQTSQDARFYAL 60
Db 1 EPAYFKEQFLDGGWTSRWIESKHKSDFGKFLVSSGKFGVDEEKDKGLQTSQDARFYAL 60
Qy 61 SASFEFNSKQTLVQVTVKHEQNIIDCGGYYVLPNSLDQTDMDHGDSEYNIMFGPDIC 120
Db 61 SASFEFNSKQTLVQVTVKHEQNIIDCGGYYVLPNSLDQTDMDHGDSEYNIMFGPDIC 120
Qy 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSLE 180
Db 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHTLYTLVIRPDNTYEVKIDNSQVESGSLE 180
RESULT 4
ID AAP92276 standard; protein; 417 AA.
XX AAP92276;
AC AAP92276;
XX 25-MAR-2003 (revised)
DT 23-FEB-1990 (first entry)
XX 60 kD Ro (Rc/SSA) antigen.
DE
XX Sjorens syndrome; systemic lupus erythematosus.
KW
XX Synthetic.
CS
XX WO8909273-A.
PN
XX 05-OCT-1989.
PD
XX 22-MAR-1989; 89WO-US001213.
PF
XX 22-MAR-1988; 88US-00171634.
PR
XX (TEXA) UNIV TEXAS SYSTEM.
PA
XX Sontheimer RD, Lieu TS, Capra JD, Mccaulliffe DP;
PI WPI; 1989-309537/42.
XX N-PSDB; AAP92276.
DR
XX DNA sequences encoding antigenic epitope(s) of Ro 60 auto-antigen -
PT used in immunoassays to detect rheumatic disease.
PT
XX Disclosure; Fig 2; 88pp; English.
PS
XX Synthetic peptides corresp. to an epitopic core of Ro antigen are
CC expressed recombinantly to detect autoantibodies, for identification of
CC

CC (e.g. diabetic neuropathy, retrorenal fibroplasia, trachoma, neovascular
 CC glaucoma, psoriasis, angiofibromas, immune inflammation.
 CC atherosclerosis, excessive wound repair, retinal neovascularization,
 CC macular degeneration, corneal graft rejection, contact lens overwear,
 CC Crohn's disease, non-immune inflammation, rheumatoid arthritis, systemic
 CC lupus erythematosus, thyroiditis, Goodpasture's syndrome, systemic
 CC vasculitis, scleroderma, Sjorgen's syndrome, sarcoidosis and primary
 CC biliary cirrhosis). The method may also be used for treating/inhibiting
 CC tumor growth especially Kaposi's sarcoma (claimed)
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 3; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDEEDKGLQTSQDARFYAL 60
 Db 18 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDEEDKGLQTSQDARFYAL 77
 QY 61 SASFEFPSNKGQTLVVQFTVKHEQNIDCGGYYVKLPFNSLDQTDHMGDSEYNIMFGPDIC 120
 Db 78 SASFEFPSNKGQTLVVQFTVKHEQNIDCGGYYVKLPFNSLDQTDHMGDSEYNIMFGPDIC 137
 QY 121 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLVTLVIRPDNTVEVKIDNSQVESGSL 180
 Db 138 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLVTLVIRPDNTVEVKIDNSQVESGSL 197

RESULT 6
 AAU77712
 ID AAU77712 standard; protein; 417 AA.
 XX
 AC AAU77712;
 XX
 DT 05-JUN-2002 (first entry)
 DE Human calreticulin (CRT).
 KW Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide;
 KW cytotaxtic; vaccine; human papillomavirus 16; HPV 16; E7; DNA vaccine;
 KW enhanced antigen-specific immune response; cytotoxic T lymphocyte;
 KW tumour; cancer; cervical cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200212281-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 02-AUG-2001; 2001WO-US024134.
 XX
 PR 03-AUG-2000; 2000US-0222902P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Wu T, Hung C;
 XX
 DR WPI; 2002-257463/30.
 DR N-PSDB; ABK11662.
 XX

PT New nucleic acids encoding a fusion polypeptide comprising an endoplasmic
 PT reticulum chaperone polypeptide linked to an antigenic polypeptide,
 PT useful as a vaccine for inducing antigen-specific immune responses.
 XX
 PS Disclosure; Page 27; 71pp; English.

CC The invention describes a nucleic acid molecule (1) encoding a fusion
 CC polypeptide comprising a first polypeptide domain comprising an
 CC endoplasmic reticulum chaperone polypeptide e.g. calreticulin (CRT) and a
 CC second polypeptide domain comprising at least one antigenic peptide e.g.
 CC Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a
 CC vaccine (DNA vaccine) for inducing enhanced antigen-specific immune

CC responses, particularly those mediated by cytotoxic T lymphocytes. The
 CC nucleic acid and compositions comprising the nucleic acid is also useful
 CC for inhibiting the growth of tumours and cancers e.g. cervical cancer.
 CC This is the amino acid sequence of the human calreticulin (CRT), an
 CC endoplasmic reticulum protein used in the creation of a DNA vaccine
 XX
 SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDEEDKGLQTSQDARFYAL 60
 Db 18 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKPYGDEEDKGLQTSQDARFYAL 77
 QY 61 SASFEFPSNKGQTLVVQFTVKHEQNIDCGGYYVKLPFNSLDQTDHMGDSEYNIMFGPDIC 120
 Db 78 SASFEFPSNKGQTLVVQFTVKHEQNIDCGGYYVKLPFNSLDQTDHMGDSEYNIMFGPDIC 137
 QY 121 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLVTLVIRPDNTVEVKIDNSQVESGSL 180
 Db 138 GPGTKKVHVFYFNKGNVLINKDIRCKDDEFTHLVTLVIRPDNTVEVKIDNSQVESGSL 197

RESULT 7
 AAE24591
 ID AAE24591 standard; protein; 417 AA.
 XX
 AC AAE24591;
 XX
 DT 04-OCT-2002 (first entry)
 DE Human calreticulin protein.
 XX
 KW Human; calreticulin; antisense compound; hyperproliferative disorder;
 KW cancer; autoimmune disease; viral infection; cardiovascular disease;
 KW antisense therapy; cytostatic; immunosuppressive; virucide.
 XX
 OS Homo sapiens.
 XX
 PN WO200236743-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 30-OCT-2001; 2001WO-US049045.
 XX
 PR 30-OCT-2000; 2000US-00702327.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Cowser LM;
 XX
 DR WPI; 2002-479759/51.
 DR N-PSDB; AAD39469.
 XX

PT Novel antisense compound targeted to nucleic acid encoding calreticulin,
 PT useful for treating a human having disease or condition associated with
 PT calreticulin e.g. cancer, viral infection, autoimmune disease.
 XX
 PS Disclosure; Page 88-90; 109pp; English.

CC The invention relates to antisense compounds, compositions and methods
 CC for modulating the expression of calreticulin. The compositions comprise
 CC antisense compounds, particularly antisense oligonucleotides, targeted
 CC to nucleic acids encoding calreticulin. The antisense compound is useful
 CC for inhibiting the expression of calreticulin in human cells or tissues.
 CC It is also useful for treating a human having a disease or condition
 CC associated with calreticulin, e.g., hyperproliferative disorder e.g.
 CC cancer, autoimmune disease, viral infection or cardiovascular disease, by
 CC inhibiting expression of calreticulin. It is useful for diagnostics, by
 CC therapeutics, prophylaxis and as research reagents and kits. It is also
 CC used in antisense therapy. The present sequence is human calreticulin

CC protein. This sequence is used in the exemplification of the invention
 XX SQ Sequence 417 AA;
 Query Match 100.0%; Score 971; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
 DB 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
 QY 61 SASPEPFSNKGQTLVQFTVKHEQNIIDCGGYYVKLPFNSLDQTMHGDSEYNIMFGPDIC 120
 DB 78 SASPEPFSNKGQTLVQFTVKHEQNIIDCGGYYVKLPFNSLDQTMHGDSEYNIMFGPDIC 137
 QY 121 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
 DB 138 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197
 RESULT 8
 ID AAE18851 standard; protein; 417 AA.
 XX AAE18851;
 AC AAE18851;
 DT 17-MAY-2002 (first entry)
 XX Human calreticulin protein.
 DE Human; prostate cancer; calreticulin; TID-1 protein; TRAITS protein;
 KW androgen action pathway; cell proliferation; kidney cancer; lymphoma;
 KW epithelium-derived carcinoma; leukaemia; vaccine; gene therapy;
 KW cytostatic; U19 protein.
 XX Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 98..170
 FT Region /label= N-terminal_domain
 FT Region 98..103
 FT Region /label= Alpha_helix
 FT Region 149..154
 FT Domain /label= Alpha_helix
 FT Domain 171..285
 FT Domain /note= "Proline-rich domain (P domain)"
 FT Domain 286..397
 FT Domain /label= C-terminal_domain
 XX WC200206327-A2.
 XX 24-JAN-2002.
 XX 17-JUL-2001; 2001WO-US022357.
 XX 17-JUL-2000; 2000US-0218761P.
 XX 16-JUL-2001; 2001US-00906393.
 XX (NOUN) UNIV NORTHWESTERN.
 XX Wang Z, Xiao W;
 PI WPI; 2002-179780/23.
 DR N-PSDB; AAD29931.
 XX Identifying a subject that is likely to have aggressive form of prostate
 PT cancer, involves comparing calreticulin levels in prostate specimen of
 PT the subject and in benign prostatic epithelial cells of the same subject.
 XX Disclosure; Page 146-148; 148pp; English.
 XX The present invention relates to methods of distinguishing aggressive

CC forms of prostate cancer from non-aggressive forms. The method involves
 CC comparing the level of calreticulin in prostate specimen and in benign
 CC prostatic epithelial cells of a subject. The invention particularly
 CC relates to two proteins, namely calreticulin and TID-1 (TRAITS; U19) that
 CC are down-regulated in aggressive forms of prostate cancer but not in
 CC slowly progressing prostate cancer. They play important roles in the part
 CC of androgen action pathway that suppresses cell proliferation and/or
 CC prevents prostate cancer. The method is useful for identifying a subject
 CC who is likely to have an aggressive form of prostate cancer. The
 CC invention further relates to a method of identifying a subject with a
 CC slow growing form of prostate cancer. TID-1 sequences are useful for
 CC treating cancers such as epithelium-derived carcinomas, kidney cancers,
 CC lymphomas, leukaemias and prostate cancers. Sequences of the invention
 CC are used as vaccines and in gene therapy. The present sequence is human
 CC calreticulin protein
 XX SQ Sequence 417 AA;
 Query Match 100.0%; Score 971; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
 DB 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
 QY 61 SASPEPFSNKGQTLVQFTVKHEQNIIDCGGYYVKLPFNSLDQTMHGDSEYNIMFGPDIC 120
 DB 78 SASPEPFSNKGQTLVQFTVKHEQNIIDCGGYYVKLPFNSLDQTMHGDSEYNIMFGPDIC 137
 QY 121 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
 DB 138 GPGTKKVHVIFNYGKGNVLINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197
 RESULT 9
 ID ABB82384 standard; protein; 417 AA.
 XX ABB82384;
 AC ABB82384;
 DT 08-JAN-2003 (first entry)
 XX Human calreticulin (CRT) protein.
 DE Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
 KW hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; CRT;
 KW calreticulin; human.
 XX Homo sapiens.
 OS WO200274920-A2.
 XX 26-SEP-2002.
 XX 18-MAR-2002; 2002WO-US008033.
 XX 16-MAR-2001; 2001US-0276854P.
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX Wu T, Hung C;
 PI WPI; 2002-740856/80.
 DR N-PSDB; ABV73173.
 XX New nucleic acid molecule encoding an antigenic fusion polypeptide useful
 PT as vaccines for enhancing or inducing immune responses, primarily
 PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
 PT tumor or viral antigens.
 XX Disclosure; Page 27; 93pp; English.
 XX

CC The invention relates to a nucleic acid molecule that encodes a fusion
 CC polypeptide, comprising a first nucleic acid sequence encoding a
 CC polypeptide that comprises at least one immunogenicity-potentiating
 CC polypeptide, optionally fused in frame with the nucleic acid, a linker
 CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
 CC in frame to them, and that encodes an antigenic peptide or polypeptide.
 CC The nucleic acid molecule, polypeptides and vectors are useful as
 CC vaccines for enhancing immune responses, primarily cytotoxic T
 CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
 CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
 CC The packaging cell line is useful for generating re-growth of a tumour.
 CC particles without contamination from replicon-competent virus. The
 CC pathogenic organisms include viruses such as human papilloma virus (HPV),
 CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
 CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
 CC as malaria, and bacteria that grow intracellularly such as mycobacteria
 CC and listeria. The present sequence represents a human calreticulin (CRT)
 XX
 XX Sequence 417 AA;

Query Match 100.0%; Score 971; DB 5; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-96;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKPVLSGGKFGYDDEKDKLQTSQDARFYAL 60
 Db 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKPVLSGGKFGYDDEKDKLQTSQDARFYAL 77

QY 61 SASFEFPSNKGQTLVVQFTVKHEQNIIDCGGVYKLPFNSLDQTDHMGDSEYNIMFGPDIC 120
 Db 78 SASFEFPSNKGQTLVVQFTVKHEQNIIDCGGVYKLPFNSLDQTDHMGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 180
 Db 138 GPGTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 10
 ABU19766
 ID ABU19766 standard; protein; 417 AA.
 XX
 AC ABU19766;
 XX
 DT 03-APR-2003 (first entry)
 DE Human MP21 protein CRTC SEQ ID NO 46.
 XX
 KW Cytostatic; p21 pathway modulating agent; cancer; angiogenic; apoptotic;
 KW cell proliferation disorder; MP21.
 OS Homo sapiens.
 XX
 PN WO2003006990-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 10-JUL-2002; 2002WO-US021549.
 XX
 PR 12-JUL-2001; 2001US-0305017P.
 PR 10-OCT-2001; 2001US-0328491P.
 PR 15-FEB-2002; 2002US-0357452P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Friedman L, Plowman GD, Belvin M, Li D, Funke RP;
 XX
 DR WPI; 2003-221779/21.
 DR N-PSDB; ABT17040.
 XX
 PT Identifying candidate p21 pathway modulator, by contacting an assay
 PT system having modifiers of p21 polypeptide or gene with a test agent to
 PT provide a reference activity in system and detecting test agent-biased
 PT activity.

XX Example; Page 153-155; 199pp; English.
 XX
 CC The invention relates to a novel method for identifying a candidate p21
 CC pathway modulating agent. The novel method comprises contacting an assay
 CC system, comprising a purified MP21 polypeptide (modifier of p21) or
 CC nucleic acid, with a test agent under conditions, so that but for the
 CC presence of a test agent, the assay system provides a reference activity
 CC and detection of test agent-biased activity of the assay system. The
 CC novel method of the invention is useful for identifying a candidate p21
 CC pathway modulating agent. The invention also includes a method for
 CC modulating the p21 pathway of a cell, and a method for diagnosing a
 CC disease e.g. cancer in a patient. The identified modulators are useful in
 CC diagnosis, therapy and pharmaceutical development. The modulators are
 CC useful in a variety of diagnostic and therapeutic applications including
 CC angiogenic, apoptotic and cell proliferation disorders. This sequence
 CC represents an MP21 protein of the invention
 XX
 XX Sequence 417 AA;

Query Match 100.0%; Score 971; DB 6; Length 417;
 Best Local Similarity 100.0%; Pred. No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKPVLSGGKFGYDDEKDKLQTSQDARFYAL 60
 Db 18 EPAVYFKEQFLDGDGWTSRWIESKHKSDFGKPVLSGGKFGYDDEKDKLQTSQDARFYAL 77

QY 61 SASFEFPSNKGQTLVVQFTVKHEQNIIDCGGVYKLPFNSLDQTDHMGDSEYNIMFGPDIC 120
 Db 78 SASFEFPSNKGQTLVVQFTVKHEQNIIDCGGVYKLPFNSLDQTDHMGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 180
 Db 138 GPGTKKVHVIFNYKGNVLIINKDIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197

RESULT 11
 AAG79824
 ID AAG79824 standard; protein; 417 AA.
 XX
 AC AAG79824;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Calreticulin.
 XX
 KW Motif; SE; signal transduction; Alzheimer's disease; neuronal cell;
 KW calreticulin; arrhythmia; idiopathic nephritic syndrome;
 KW non-autoimmune hyperthyroidism; obesity; polycystic kidney disease;
 KW cancer; asthma; atopic dermatitis; psoriasis; rheumatoid arthritis;
 KW systemic lupus erythematosus; infectious disease; atherosclerosis;
 KW inflammatory bowel disease; osteoarthritis; septic shock;
 KW ischaemia-reperfusion injury.
 XX
 OS Homo sapiens.
 XX
 PN WO200299061-A2.
 XX
 PD 12-DEC-2002.
 XX
 PF 04-JUN-2002; 2002WO-US017536.
 XX
 PR 04-JUN-2001; 2001US-0295691P.
 PR 03-JUN-2002; 2002US-00161959.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Holoshitz J, Ling S;
 XX
 DR WPI; 2003-156853/15.

PT Treating diseases associated with signal transduction aberrations, e.g.
PT Alzheimer's disease, arrhythmia or rheumatoid arthritis, comprises
PT administering a preparation comprising an SE- or an SE motif-containing
PT peptide.
XX
PS Disclosure; Fig 14; 97pp; English.
XX
XX This sequence represents human calreticulin. This protein was used in the
CC method of the invention for treating diseases associated with signal
CC transduction aberrations. The method comprises: (a) providing a subject
CC with one or more symptoms of Alzheimer's disease and, optionally, a
CC plurality of neuronal cells expressing calreticulin, and a preparation
CC comprising an shared epitope (SE)- containing peptide or a peptide which
CC binds the calreticulin; and (b) administering the preparation to the
CC subject. The inventive method is useful for treating diseases associated
CC with signal transduction aberrations, such as Alzheimer's disease,
CC arrhythmia, idiopathic nephritic syndrome, non-autoimmune
CC hyperthyroidism, obesity, polycystic kidney disease, cancer, asthma,
CC atopic dermatitis, psoriasis, rheumatoid arthritis, systemic lupus
CC erythematosus, infectious diseases, inflammatory bowel disease,
CC osteoarthritis, septic shock, atherosclerosis, congestive heart failure,
CC insulin-resistance syndrome, and ischaemia-reperfusion injury
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-98;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60
Db 18 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 77
QY 61 SASFEPFNKGOTLVQFTVKHEONIDCGGVYKLPFNSLDQTDHGDSEYNIMFGPDIC 120
Db 78 SASFEPFNKGOTLVQFTVKHEONIDCGGVYKLPFNSLDQTDHGDSEYNIMFGPDIC 137
QY 121 GPGTKKVHVIFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 180
Db 138 GPGTKKVHVIFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 12
ADA26337
ID ADA26337 standard; protein; 417 AA.
XX
AC ADA26337;
XX
XX Human calreticulin protein SEQ ID NO:14.
DE
DE stress response protein; immune response; tumour;
KW tumour growth inhibition; metastasis; cytostatic; vaccine; gene therapy;
KW human; calreticulin.
KW
XX Homo sapiens.
XX WO2003068941-A2.
XX
XX 21-AUG-2003.
XX
XX 13-FEB-2003; 2003WO-US004631.
XX
XX 13-FEB-2002; 2002US-0356293P.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Nicchita C, Baker-Lepain J;
XX
XX WPI; 2003-679635/64.
XX
XX N-PSDB; ADA26336.
XX

PT New Hsp60, Hsp70, Hsp90 or calreticulin polypeptide, useful for preparing
PT a composition for inhibiting tumor growth or metastasis in a subject.
XX
PS Disclosure; Page 137-138; 150pp; English.
XX
XX The present invention describes a recombinant stress response polypeptide
CC (I) free of an antigen-binding domain, where the recombinant stress
CC response polypeptide comprises an extracellularly transported polypeptide
CC when expressed in a host cell. Also described: (1) a composition for
CC eliciting an immune response in a subject; (2) eliciting an immune
CC response in a subject; and (3) inhibiting tumour growth or metastasis in
CC a subject. (I) has cytostatic activity, and can be used in vaccines and
CC in gene therapy. The polypeptide (I) can be used for preparing a
CC composition for inhibiting tumour growth or metastasis in a subject. The
CC present sequence represents human calreticulin, which is a stress
CC response polypeptide given in the exemplification of the present
CC invention.
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 6; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-98;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 60
Db 18 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDGLQTSQDARFYAL 77
QY 61 SASFEPFNKGOTLVQFTVKHEONIDCGGVYKLPFNSLDQTDHGDSEYNIMFGPDIC 120
Db 78 SASFEPFNKGOTLVQFTVKHEONIDCGGVYKLPFNSLDQTDHGDSEYNIMFGPDIC 137
QY 121 GPGTKKVHVIFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 180
Db 138 GPGTKKVHVIFNYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 13
ADD22407
ID ADD22407 standard; protein; 417 AA.
XX
AC ADD22407;
XX
XX 15-JAN-2004 (first entry)
XX
XX HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 57.
DE
DE tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
KW colon; mouth; lung; prostatic; gynecological; human.
KW
XX Homo sapiens.
XX
XX JP2003111595-A.
XX
XX 15-APR-2003.
XX
XX 24-JUN-2002; 2002JP-00183603.
XX
XX 25-JUN-2001; 2001JP-00191974.
XX
XX (ITOY/) ITO Y.
XX
XX WPI; 2003-611129/58.
XX
XX Novel tumor antigenic peptide or polypeptide useful for inducing
PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
PT prostatic or gynecological cancer.
PT
XX Claim 2; SEQ ID NO 57; 98pp; Japanese.
XX
XX The invention relates to a novel tumour antigenic peptide or polypeptide
CC comprising a sequence selected from 99 sequences fully defined in the
CC specification. The tumour antigenic peptide or polypeptide comprises a
CC

CC sequence selected from 99 sequences fully defined in the specification,
 CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
 CC Pro-Leu-Ser-Gln-Glu-Thr-Phe, and the polypeptide preferably has a
 CC sequence comprising 393 amino acids fully defined in the specification.
 CC The invention further provides a cancer vaccine comprising a tumour
 CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
 CC antigenic peptide, polypeptide, its encoding polynucleotide, a
 CC hybridising polynucleotide, a recombinant vector containing the
 CC polynucleotide, a host transformed with the vector or an antibody are
 CC useful for screening for compounds that interact with the tumour
 CC antigenic peptide, the polypeptide or its encoding polynucleotide and
 CC increases the expression of the tumour antigenic peptide, the polypeptide
 CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
 CC useful for inducing cytotoxic T cells. The tumour antigenic peptide is
 CC vaccine is useful for treating cancer such as colon, mouth, lung,
 CC prostatic or gynecological cancer. The invention also provides a
 CC pharmaceutical composition useful for treating cancer. The tumour
 CC antigenic peptide or the polypeptide is useful as an antigen to create
 CC antibodies. This sequence represents one of the tumour antigenic
 CC polypeptides of the invention.

XX SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 7; Length 417;
 Best Local Similarity 100.0%; Pred No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSMWESKHSDFGKFLVSGKFGYDGEKDKGLQTSQDARFYAL 60
 Db 18 EPAVYFKEQFLDGDGWTSMWESKHSDFGKFLVSGKFGYDGEKDKGLQTSQDARFYAL 77
 QY 61 SASFEPFSNKGOTLVVQFTVKHEQNTDCGGVYVKLPFNSLDQTMHGDSEYNIMFGPDIC 120
 Db 78 SASFEPFSNKGOTLVVQFTVKHEQNTDCGGVYVKLPFNSLDQTMHGDSEYNIMFGPDIC 137
 QY 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 Db 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 14
 ADE56308
 ID ADE56308 standard; protein; 417 AA.

XX ADE56308;

XX 29-JAN-2004 (first entry)

XX Human Protein NP_004334, SEQ ID NO 2160.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; NP_004334.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 7; Length 417;
 Best Local Similarity 100.0%; Pred No. 1.4e-98;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAVYFKEQFLDGDGWTSMWESKHSDFGKFLVSGKFGYDGEKDKGLQTSQDARFYAL 60
 Db 18 EPAVYFKEQFLDGDGWTSMWESKHSDFGKFLVSGKFGYDGEKDKGLQTSQDARFYAL 77
 QY 61 SASFEPFSNKGOTLVVQFTVKHEQNTDCGGVYVKLPFNSLDQTMHGDSEYNIMFGPDIC 120
 Db 78 SASFEPFSNKGOTLVVQFTVKHEQNTDCGGVYVKLPFNSLDQTMHGDSEYNIMFGPDIC 137
 QY 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
 Db 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 15
 ADE56312

ID ADE56312 standard; protein; 417 AA.

XX ADE56312;

XX 29-JAN-2004 (first entry)

XX Human Protein NP_004334, SEQ ID NO 2164.

XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR GENBANK; NP_004334.
XX
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 417 AA;

Query Match 100.0%; Score 971; DB 7; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.4e-98;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EPAYVFEQFLDGGWTSRMIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
Db 18 EPAYVFEQFLDGGWTSRMIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 77

Qy 61 SASPEFSPNKGQTLVQFTVKHEQNDICGGGYVKLPFNSLDQTDMDHGDSEYNIMFGPDIC 120
Db 78 SASPEFSPNKGQTLVQFTVKHEQNDICGGGYVKLPFNSLDQTDMDHGDSEYNIMFGPDIC 137

Qy 121 GPGTKKVVIVNYGKGNVLINKDRCXDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 180
Db 138 GPGTKKVVIVNYGKGNVLINKDRCXDDETHLYTLIVRPDNTYEVKIDNSQVESGSL 197

Search completed: October 15, 2004, 13:15:38
Job time : 159 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 15, 2004, 13:11:18 ; Search time 21 Seconds
(without alignments)
568.440 Million cell updates/sec

Title: US-09-807-148-4
Perfect score: 971
Sequence: 1 EPAYFKEQFLDGDGWTSRW.....PNTYEVKIDNSQVSGSLE 180
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	180	4	US-09-828-000-3
2	971	100.0	416	4	US-09-828-000-2
3	971	100.0	417	4	US-09-538-092-1023
4	971	100.0	417	4	US-09-906-393A-36
5	527	54.3	415	3	US-08-675-816-2
6	494	50.9	420	4	US-09-844-006A-2
7	340	35.0	61	4	US-09-828-000-4
8	327	33.7	61	4	US-09-828-000-8
9	290	29.9	593	1	US-08-236-362-2
10	288	29.7	592	4	US-09-538-092-1024
11	261	26.9	610	4	US-09-976-594-947
12	230	23.7	230	4	US-09-248-796A-14160
13	227.5	23.4	542	3	US-08-675-816-6
14	189	19.5	35	4	US-09-828-000-7
15	151	15.6	27	4	US-09-828-000-5
16	114.5	11.8	162	4	US-09-513-999C-4228
17	114.5	11.8	162	4	US-09-513-999C-4229
18	101	10.4	867	4	US-10-140-002-20
19	97	10.0	690	4	US-09-886-319A-36
20	96	9.9	18	4	US-09-828-000-6
21	89	9.2	660	3	US-09-181-706-8
22	89	9.2	660	3	US-09-458-791-8
23	89	9.2	660	3	US-09-439-066-8
24	89	9.2	660	4	US-09-459-065-8
25	81	8.3	261	4	US-09-252-991A-28346
26	81	8.3	307	4	US-09-810-347-5
27	81	8.3	360	4	US-09-810-347-4

28	81	8.3	372	4	US-09-810-347-2	Sequence 2, Appli
29	81	8.3	871	4	US-09-773-426A-3	Sequence 3, Appli
30	81	8.3	871	4	US-10-314-881-3	Sequence 3, Appli
31	81	8.3	871	4	US-09-495-823-3	Sequence 16, Appli
32	81	8.3	1611	4	US-09-668-673B-16	Sequence 16, Appli
33	81	8.3	1611	4	US-10-389-532-16	Sequence 48, Appli
34	77.5	8.0	642	2	US-08-245-511-48	Sequence 48, Appli
35	77.5	8.0	642	2	US-08-600-993A-48	Sequence 2948, Ap
36	77.5	8.0	661	4	US-09-583-110-2948	Sequence 53, Appli
37	77	7.9	15	3	US-08-946-026-53	Sequence 14203, A
38	76	7.8	107	4	US-09-248-796A-14203	Sequence 4701, App
39	76	7.8	360	4	US-09-538-092-471	Sequence 8, Appli
40	76	7.8	501	3	US-09-157-257-8	Sequence 2443, Ap
41	75.5	7.8	699	4	US-09-540-236-2443	Sequence 2, Appli
42	75.5	7.8	867	4	US-09-668-673B-2	Sequence 2, Appli
43	75.5	7.8	867	4	US-10-389-532-2	Sequence 4, Appli
44	75	7.7	591	3	US-08-931-408-4	Sequence 4, Appli
45	75	7.7	591	3	US-09-432-473-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-828-000-3
; Sequence 3, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 971; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 8.5e-102;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
DB 1 EPAYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEKDKGLQTSQDARFYAL 60
QY 61 SASFPFSGKGTLLVQFTVKHEQNI DCGGGVVKLF PMSLDQTMHGDSEYNI MEGPDIC 120
DB 61 SASFPFSGKGTLLVQFTVKHEQNI DCGGGVVKLF PMSLDQTMHGDSEYNI MEGPDIC 120
QY 121 GFGTKKHVIFNYKGNVLI NKDKRCKDDEFTHTLYTLVLRPNTYEVKIDNSQVSGSLE 180
DB 121 GFGTKKHVIFNYKGNVLI NKDKRCKDDEFTHTLYTLVLRPNTYEVKIDNSQVSGSLE 180

RESULT 2
US-09-828-000-2
; Sequence 2, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT

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; ORGANISM: Calreticulin
US-09-828-000-2

Query Match      100.0%; Score 971; DB 4; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.8e-101;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77

QY 61 SASFEPFSNKGQTLVVQFTVKHEQNDICGGGYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASFEPFSNKGQTLVVQFTVKHEQNDICGGGYVKLFPNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 180
DB 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 197

RESULT 3
US-09-538-092-1023
; Sequence 1023, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538, 092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CukaPatSeqFormatter Version 0.9
; SEQ ID NO 1023
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P27797
US-09-538-092-1023

Query Match      100.0%; Score 971; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.9e-101;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77

QY 61 SASFEPFSNKGQTLVVQFTVKHEQNDICGGGYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASFEPFSNKGQTLVVQFTVKHEQNDICGGGYVKLFPNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 180
DB 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 197

RESULT 4
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Patent No. 6780984
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
```

```
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

Query Match      100.0%; Score 971; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 2.9e-101;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYVFKQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYGDDEKDKGLQTSQDARFYAL 77

QY 61 SASFEPFSNKGQTLVVQFTVKHEQNDICGGGYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASFEPFSNKGQTLVVQFTVKHEQNDICGGGYVKLFPNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 180
DB 138 GPGTKKVHVIFNYKGNVNLINKDIRCKDDEFTHLTYTLIVRPDNTYEVKIDNSQVSSGLE 197

RESULT 5
US-08-675-816-2
; Sequence 2, Application US/08675816
; Patent No. 6171864
; GENERAL INFORMATION:
; APPLICANT: Coughlan, Sean J.
; APPLICANT: Winfrey, Jr., Ron J.
; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 701 Fifth Ave. Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,816
; FILING DATE: 05-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6171864tenburg, Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 750027.401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)-622-4900
; TELEFAX: (206)-682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-675-816-2

Query Match      54.3%; Score 527; DB 3; Length 415;
Best Local Similarity 55.3%; Pred. No. 4.8e-51;
Matches 99; Conservative 31; Mismatches 43; Indels 6; Gaps 3;
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Qy	4	VYFKQFLDGDQWTSWETSHKSD---FGKVLSSCKFYGDDEKKGIGTQSDARFYAL	60
Db	22	VFEERF--EDGWNRWYSQWKDENTAGWNVTSGKNGD--PNDKGTQSDYRYFAL	78
Qy	61	SASFPFNNKGOTLVQVTVKHEQNI DCGGYVKLPNSLDQTDMMHGDSEYNI MFGPDIC	120
Db	79	SAEFPFNNKQTLTVQFESVHEQKLD CGGYMKLLSSTDQKFGGDTFYSIMFGPDIC	138
Qy	121	GGCTKKVHVI FNYKGNVLINKIRCKDDETHLYTLIVRPDNTYEVKIDNSQVESGSL	179
Db	139	GYSTKKVHAI LNYDNTNHLIKVEPCETDQTHVTLIVIFEDATYSILIDNVEKQTGSL	197

```

RESULT 6
US-09-844-006A-2
; Sequence 2, Application US/09844006A
; Patent No. 6753462
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Zea mays
US-09-844-006A-2

```

	Query Match	50.9%;	Score 494;	DB 4;	Length 420;	
	Best Local Similarity	53.1%;	Pred. No. 2.6e-47;			
	Matches	95;	Conservative 32;	Mismatches 46;	Indels 6;	Gaps 3;
Qy	4	VYPKEQLDGGWTSRMIESKHKD---	FGFVLVSSGFYGDDEKGLQTSQDAFFVAL	60		
		: :: :: :	::: :	:	:	:
Dd	27	VFFQEKF--EDGWESRWYKSWKKDENNAGEWNHTSGKWNGDAE-DKGIQISETDYRFVAI	83			
		: :: :: :	::: :	:	:	:
Qy	61	SASPEPSNKGQTILVQPTVKHEQNIDCGGVYKLFPNSLDQTMHGSDSEYNINFGPDIC	120			
		: :: :: :	::: :	:	:	:
Dd	84	SAETPEPSNKDKTILVLPQSFKHEQKLDCGGYVKLLGGDVQKTLGGDTSVSIIISRPDIS	143			
		: :: :: :	::: :	:	:	:
Qy	121	GPFGTKKHVIENYRGNKLVINKDRCKODEPETHYLTVLRPDNTVEYKDINSQVESGSL	179			
		: :: :: :	::: :	:	:	:
b	144	EVSSTKVTHITLTKGKNHILKEDVPCTMDQTHVTFLIRPDATSYLIIDEKREKHTGSI	202			
		: :: :: :	::: :	:	:	:

RESULT 7
 US-09-828-000-4
 ; Sequence 4, Application US/09828000
 ; Patent No. 6596690
 ; GENERAL INFORMATION:
 ; APPLICANT: Government of the United States of America
 ; TITLE OF INVENTION: Vasostatin as Marrow Protectant
 ; FILE REFERENCE: 4239-55414
 ; CURRENT APPLICATION NUMBER: US/09/828,000
 ; CURRENT FILING DATE: 2001-04-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 61
 ; TYPE: PRT
 ; ORGANISM: Fragment 1
 US-09-828-000-4

Query Match 35.0%; Score 340; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;

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Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 103 TDMHGDSEYNINFGPDICGPGTKKVHVIIFYKGNVLINKDIRCKDDFTHLYTLIVRPD 162
Db 1 TDMHGDSEYNINFGPDICGPGTKKVHVIIFYKGNVLINKDIRCKDDFTHLYTLIVRPD 60
Qy 163 N 163
Db 61 N 61

RESULT 8
US-09-828-000-8
; Sequence 8, Application US/09828000
; Patent No. 6596690
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasoctatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Fragment 5
US-09-828-000-8

Query Match 33.7%; Score 327; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	120	CGGTGKXHVIFNYKGNVLIN	KDTRCKDDPETHLYTLIV	RPDNTYEVKIDNSQVESGSL	179
Db	1	CGGTGKXHVIFNYKGNVLIN	KDTRCKDDPETHLYTLIV	RPDNTYEVKIDNSQVESGSL	60
Qy	180	E	180		
Db	61	E	61		

RESULT 9
 US-08-296-362-2
 ; Sequence 2, Application US/08296362
 ; Patent No. 5691306
 ; GENERAL INFORMATION:
 ; APPLICANT: Bergeron, John J.M.
 ; APPLICANT: Thomas, David Y.
 ; APPLICANT: Wada, Ikuc
 ; TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF
 ; TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING SECRETORY
 ; TITLE OF INVENTION: PROTEIN PRODUCTION
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: US
 ; ZIP: 98104-7092
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/296,362
 ; FILING DATE: 25-AUG-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deehr, Manya S.
 ; REGISTRATION NUMBER: 37,120

REFERENCE/DOCKET NUMBER: 690066.401C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 TELEX: 3723836
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 593 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-296-362-2

Query Match 29.9%; Score 290; DB 1; Length 593;
 Best Local Similarity 38.1%; Pred. No. 5.2e-24;
 Matches 77; Conservative 26; Mismatches 65; Indels 34; Gaps 9;
 QY 4 VYFKEQFLDGDGWTSGRWIESKHKSD-----FGKVLSSGKFGYGDDEK-----DKGLQTS 52
 DB 70 VYFADSF--DRGTLSCWILSKAKKDDTDDEIAKY---DGKWEVDENKTKLPDGKGLVLM 124
 QY 53 QDARFYALSASF-EFNSKNGQTLVQFTVYKHEQNIIDCGGYVKLPFN-----SLDQTDWHG 107
 DB 125 SRKHHAISAKLNKPLFDTKPLIVQYEVNFQNGIECGGAYVKLLSKTPELNLDQ--FHD 182
 QY 108 DSEYNIMFGPDICGPGTKKVVHIFNYKGNKVLINKDIRCK-----DDEFTHLTYL 157
 DB 183 KTYPTIMFGPKCGE-DYKLFHIFRHKNPKTGYEKKHAKRPDADLKTYFTDKKTHLYL 241
 QY 158 IVRPNTYEVKIDNSQVESGSL 179
 DB 242 ILNPDNSFEILVDQSVVNSGNL 263

RESULT 10

US-09-538-092-1024
 Sequence 1024; Application US/09538092
 Patent No. 6753314
 GENERAL INFORMATION:
 APPLICANT: Glot, Loic
 APPLICANT: Mansfield, Traci A.
 TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 FILE REFERENCE: 15966-542
 CURRENT APPLICATION NUMBER: US/09/538,092
 CURRENT FILING DATE: 2000-03-29
 PRIOR APPLICATION NUMBER: 60/127,352
 PRIOR FILING DATE: 1999-04-01
 PRIOR APPLICATION NUMBER: 60/178,965
 PRIOR FILING DATE: 2000-02-01
 NUMBER OF SEQ ID NOS: 1387
 SOFTWARE: CuraPatSeqformatter Version 0.9
 SEQ ID NO 1024
 LENGTH: 592
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (0)...(0)
 OTHER INFORMATION: Polypeptide Accession Number P27824
 US-09-538-092-1024

Query Match 29.7%; Score 288; DB 4; Length 592;
 Best Local Similarity 38.1%; Pred. No. 8.7e-24;
 Matches 77; Conservative 26; Mismatches 65; Indels 34; Gaps 9;
 QY 4 VYFKEQFLDGDGWTSGRWIESKHKSD-----FGKVLSSGKFGYGDDEK-----DKGLQTS 52
 DB 69 VYFADSF--DRGTLSCWILSKAKKDDTDDEIAKY---DGKWEVDENKTKLPDGKGLVLM 123
 QY 53 QDARFYALSASF-EFNSKNGQTLVQFTVYKHEQNIIDCGGYVKLPFN-----SLDQTDWHG 107
 DB 124 SRKHHAISAKLNKPLFDTKPLIVQYEVNFQNGIECGGAYVKLLSKTPELNLDQ--FHD 181

QY 108 DSEYNIMFGPDICGPGTKKVVHIFNYKGNKVLINKDIRCK-----DDEFTHLTYL 157
 DB 182 KTYPTIMFGPKCGE-DYKLFHIFRHKNPKTGYEKKHAKRPDADLKTYFTDKKTHLYL 240
 QY 158 IVRPNTYEVKIDNSQVESGSL 179
 DB 241 ILNPDNSFEILVDQSVVNSGNL 262

RESULT 11

US-09-976-594-947
 Sequence 947; Application US/09976594
 Patent No. 6673549
 GENERAL INFORMATION:
 APPLICANT: Furness, Michael
 APPLICANT: Buchbinder, Jenny
 TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 FILE REFERENCE: PA-0041 US
 CURRENT APPLICATION NUMBER: US/09/976,594
 CURRENT FILING DATE: 2001-10-12
 PRIOR APPLICATION NUMBER: 60/240,409
 PRIOR FILING DATE: 2000-10-12
 NUMBER OF SEQ ID NOS: 1143
 SOFTWARE: PERL Program
 SEQ ID NO 947
 LENGTH: 610
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No. 6673549 3876162CD1
 US-09-976-594-947

Query Match 26.9%; Score 261; DB 4; Length 610;
 Best Local Similarity 34.5%; Pred. No. 1e-20;
 Matches 68; Conservative 33; Mismatches 72; Indels 24; Gaps 7;

QY 4 VYFKEQFLDGDGWTSGRWIESKHKSD--FGKVLSSGKFGYGDDEK-----DKGLQTSODA 55
 DB 60 VYFAETF--DSGRLAGWLSKAKKDDMDDEISYDGRWEIEELKENQVPGDGLVKSR 117
 QY 56 RFVALSASF-EFNSKNGQTLVQFTVYKHEQNIIDCGGYVKLPFNSLD--QTMHGDSEYN 112
 DB 118 KHAISAVLAKPFIADKPLIVQYEVNFQDGGAYIKLADTDDLLILENFYDKTSYI 177
 QY 113 IMFPGDPCGPGTKKVVHIFNYKGNKVLINKDIRCK-----DDEFTHLTYLIVRPD 162
 DB 178 IMFPGPKCGE-DYKLFHIFRHKNPKTGYEKKHAKRPDADLKTYFTDKKTHLYLVMNPD 236
 QY 163 NTYEVKIDNSQVESGSL 179
 DB 237 DTFEVLVDQTVVNSGNL 253

RESULT 12

US-09-248-796A-14160
 Sequence 14160; Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstein et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 14160
 LENGTH: 230
 TYPE: PRT

ORGANISM: Candida albicans
US-09-248-796A-14160
Query Match 23.7%; Score 230; DB 4; Length 230;
Best Local Similarity 32.0%; Pred. No. 8.1e-18;
Matches 66; Conservative 39; Mismatches 69; Indels 32; Gaps 10;
QY 1 EPAVYFKEQF---LDCDGTSTRWIESKHKSDFGK--FVLSGKF-----YGDDEKD 46
DB 27 DPSSVP-EQPDYSLNSPPQ---VSTAKKFDGDRDEIVRYSGEWKIESSTSKYPCLEGD 82
QY 47 KGLQTSQDARFALS-----ASPEPFSKNGQTLVVQFTVKHEQNIIDCGGCVKLPFNS 99
DB 83 LGLVMKSRASHYAISYKLPHEVTNPNNTQDLVLOYEVKLQGLTCGGAYIKLDDSS 142
QY 100 -LQDTMHGDSYNIIMFGPDICGPGTKKHVIFNYKGNVLI-NKDIR-----CKDEFTH 153
DB 143 PSYGKFNSTPQIMFGPVCV-SENKHFIFIRKLPNGAIBEKHLKHKPMARTNELN 201
QY 154 LYTLIVRPNTYRKVDNSQVSGSL 179
DB 202 LYTLIIKFNDSFIRINGTVAKAGNL 227
RESULT 13
US-08-675-816-6
Query Match 23.4%; Score 227.5; DB 3; Length 542;
Best Local Similarity 36.0%; Pred. No. 5.4e-17;
Matches 64; Conservative 24; Mismatches 73; Indels 17; Gaps 10;
QY 6 FKEQFLDGDGWTSTRWIESKHKSDFGKFLVSSGKFGYDDEKDKGLQTSQDARFALSASF- 64
DB 35 FYESF--EDSPEGRWTLISA-KDDY-KGEWKHAKSEGHDE--YGLLVSEKARKVAIVKELD 88
QY 65 EPPFNKQGTLLVQFTVKHEQNIIDCGGGYVK-LFPNSLDQT--DMHGDSEYNIIMFGPDICG 121

US-09-828-000-7
Sequence 7, Application US/09828000
Patent No. 6596690
GENERAL INFORMATION:
APPLICANT: Government of the United States of America
TITLE OF INVENTION: Vasostatin as Marrow Protectant
FILE REFERENCE: 4239-55414
CURRENT APPLICATION NUMBER: US/09/828,000
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in version 3.0
SEQ ID NO 7
LENGTH: 35
TYPE: PRT
ORGANISM: Fragment 4
US-09-828-000-7
Query Match 19.5%; Score 189; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 129 VIFNYKGNVLIINCKIRCKDDDEFTHLYTLIVRPDN 153
DB 1 VIFNYKGNVLIINCKIRCKDDDEFTHLYTLIVRPDN 35
RESULT 15
US-09-828-000-5
Sequence 5, Application US/09828000
Patent No. 6596690
GENERAL INFORMATION:
APPLICANT: Government of the United States of America
TITLE OF INVENTION: Vasostatin as Marrow Protectant
FILE REFERENCE: 4239-55414
CURRENT APPLICATION NUMBER: US/09/828,000
CURRENT FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patent in version 3.0
SEQ ID NO 5
LENGTH: 27
TYPE: PRT
ORGANISM: Fragment 2
US-09-828-000-5
Query Match 15.6%; Score 151; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.2e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 120 CGPGTKKHVIFNYKGNVLIINCKIRCKDDDEFTHLYTLIVRPDN 146
DB 1 CGPGTKKHVIFNYKGNVLIINCKIRCKDDDEFTHLYTLIVRPDN 27
Search completed: October 15, 2004, 13:16:02
Job time : 22 secs

US-08-675-816-6
Sequence 6, Application US/08675816
Patent No. 6171864
GENERAL INFORMATION:
APPLICANT: Coughlan, Sean J.
APPLICANT: Winfrey, Jr. Ron J.
TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 701 Fifth Ave. Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,816
FILING DATE: 05-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6171864tenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 750027.401
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206-622-4900
TELEFAX: (206)-682-6031
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-675-816-6

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 15, 2004, 13:12:37 ; Search time 49 Seconds
(without alignments)
1187.702 Million cell updates/sec

Title: US-09-807-148-4
Perfect score: 971
Sequence: 1 EPAYFKQFLDGDGWTSRW.....PNTYEVKIDNSQVSGSLE 180

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 32331874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/prodata1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata1/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata1/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/prodata1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/prodata1/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/prodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	971	100.0	180	10	US-09-828-000-3
2	971	100.0	180	14	US-10-405-588-3
3	971	100.0	416	10	US-09-828-000-2
4	971	100.0	416	14	US-10-405-588-2
5	971	100.0	417	10	US-09-906-393A-36
6	971	100.0	417	14	US-10-161-959-29
7	971	100.0	417	14	US-10-367-093-14
8	933	96.1	416	14	US-10-316-253-2
9	933	96.1	416	14	US-10-316-253-4
10	933	96.1	416	14	US-10-316-253-6
11	631	65.0	390	14	US-10-161-927-46
12	619.5	63.8	395	14	US-10-369-493-6343
13	616.5	63.5	177	15	US-10-264-049-3546
14	584	60.1	210	16	US-10-767-701-55877

15	536	55.2	435	15	US-10-425-114-70304	Sequence 70304, A
16	530	54.6	421	16	US-10-767-701-46544	Sequence 46544, A
17	529	54.5	442	16	US-10-437-963-114914	Sequence 114914, A
18	529	54.5	667	16	US-10-437-963-114860	Sequence 114860, A
19	527	54.3	424	16	US-10-437-963-201427	Sequence 201427, A
20	526	54.2	424	16	US-10-437-963-201420	Sequence 201420, A
21	523.5	53.9	388	15	US-10-425-114-46405	Sequence 46405, A
22	523.5	53.9	391	15	US-10-425-114-69619	Sequence 69619, A
23	523.5	53.9	442	15	US-10-425-114-46869	Sequence 46869, A
24	517	53.2	420	15	US-10-424-599-190958	Sequence 190958, A
25	512	52.7	431	16	US-10-767-701-44015	Sequence 44015, A
26	503	51.8	391	15	US-10-424-599-190956	Sequence 190956, A
27	503	51.8	391	15	US-10-425-114-46228	Sequence 46228, A
28	503	51.8	391	15	US-10-425-114-55395	Sequence 55395, A
29	494	50.9	420	9	US-09-844-006A-2	Sequence 2, Appli
30	489	50.4	425	16	US-10-437-963-122222	Sequence 122222, A
31	483	49.7	290	15	US-10-425-114-44768	Sequence 44768, A
32	483	49.7	434	15	US-10-425-114-70140	Sequence 70140, A
33	483	49.7	439	15	US-10-425-114-65495	Sequence 65495, A
34	479	49.3	422	15	US-10-424-599-277445	Sequence 277445, A
35	476	49.0	279	16	US-10-767-701-39041	Sequence 39041, A
36	468	48.2	422	16	US-10-767-701-45264	Sequence 45264, A
37	467	48.1	247	15	US-10-424-599-153809	Sequence 153809, A
38	466	48.0	372	15	US-10-425-114-44621	Sequence 44621, A
39	466	48.0	372	15	US-10-425-114-54997	Sequence 54997, A
40	466	48.0	418	15	US-10-424-599-153808	Sequence 153808, A
41	465.5	47.9	993	16	US-10-437-963-114903	Sequence 114903, A
42	460	47.4	434	15	US-10-425-114-57598	Sequence 57598, A
43	438	45.1	161	16	US-10-767-701-61035	Sequence 61035, A
44	421	43.4	346	15	US-10-425-114-48930	Sequence 48930, A
45	340	35.0	61	10	US-09-828-000-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-828-000-3
; Sequence 3, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-09-828-000-3

Query Match 100.0%; Score 971; DB 10; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	EPAYFKQFLDGDGWTSRWIESKHSDFGKFLSSGKFGYGDDEKDKGLQTSQDARFYAL	60
Db	1	EPAYFKQFLDGDGWTSRWIESKHSDFGKFLSSGKFGYGDDEKDKGLQTSQDARFYAL	60
Qy	61	SASFPFNNKGQTLVVOFTVHQEQNIDCGGKVKLFNLSLQTDHMGDSEYNIMEGPDIC	120
Db	61	SASFPFNNKGQTLVVOFTVHQEQNIDCGGKVKLFNLSLQTDHMGDSEYNIMEGPDIC	120
Qy	121	PGGTKKVHVFNYKGNVINKDKIRCKDDEFTHTLTVRPDNTYEVKIDNSQVSGSLE	180
Db	121	PGGTKKVHVFNYKGNVINKDKIRCKDDEFTHTLTVRPDNTYEVKIDNSQVSGSLE	180

RESULT 2

US-10-405-588-3

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; Sequence 3, Application US/10405588
; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Vasostatin
US-10-405-588-3

Query Match      100.0%; Score 971; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.8e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
DB 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60

QY 61 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 61 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120

QY 121 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
DB 121 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 180

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RESULT 3
US-09-828-000-2
; Sequence 2, Application US/09828000
; Publication No. US20030078198A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/09/828,000
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-09-828-000-2

Query Match      100.0%; Score 971; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.6e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 77

QY 61 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
DB 138 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 4
US-10-405-588-2
; Sequence 2, Application US/10405588

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; Publication No. US20030216299A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America
; TITLE OF INVENTION: Vasostatin as Marrow Protectant
; FILE REFERENCE: 4239-55414
; CURRENT APPLICATION NUMBER: US/10/405,588
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: US/09/828,000
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Calreticulin
US-10-405-588-2

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Query Match      100.0%; Score 971; DB 14; Length 416;
Best Local Similarity 100.0%; Pred. No. 5.6e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 77

QY 61 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
DB 138 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

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RESULT 5
US-09-906-393A-36
; Sequence 36, Application US/09906393A
; Publication No. US20030039970A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Zhou
; APPLICANT: Xiao, Wuhan
; TITLE OF INVENTION: METHOD OF PROGNOSING CANCER AND THE PROTEINS INVOLVED
; FILE REFERENCE: 1720-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/906,393A
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/218,761
; PRIOR FILING DATE: 2000-07-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-906-393A-36

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Query Match      100.0%; Score 971; DB 10; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.6e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 60
DB 18 EPAYVKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFYGDDEKDKGLQTSQDARFYAL 77

QY 61 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASPEFSSNKGQTLVQVFTVKHEQNIIDCGGYYVKLFPNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 180
DB 138 GPGTKKVHVFYFNKGNVNLINKDIRCKDEFFHLYTLIVRPDNTYEVKIDNSQVESGSLE 197

RESULT 6

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US-10-161-959-29
; Sequence 29, Application US/10161959
; Publication No. US20030096748A1
; GENERAL INFORMATION:
; APPLICANT: Holoshitz, Joseph
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Diseases Associated
; FILE REFERENCE: UM-07135
; CURRENT APPLICATION NUMBER: US/10/161,959
; CURRENT FILING DATE: 2002-10-01
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 29
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-161-959-29

Query Match 100.0%; Score 971; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.6e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
DB 18 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
QY 61 SASFEPSNKGQTLVQVFTVKHEQNDICCGGVYKLPFNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASFEPSNKGQTLVQVFTVKHEQNDICCGGVYKLPFNSLDQTMHGDSEYNIMFGPDIC 137
QY 121 GPGTKKVHVIENYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIENYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 7
US-10-367-093-14
; Sequence 14, Application US/10367093
; Publication No. US20030216315A1
; GENERAL INFORMATION:
; APPLICANT: Duke University
; APPLICANT: Nicchitta, Chris
; APPLICANT: Baker-LePain, Julie
; TITLE OF INVENTION: MODULATION OF IMMUNE RESPONSE BY NON-PEPTIDE BINDING STRESS RESP
; FILE REFERENCE: 180/145
; CURRENT APPLICATION NUMBER: US/10/367,093
; CURRENT FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 14
; LENGTH: 417
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-093-14

Query Match 100.0%; Score 971; DB 14; Length 417;
Best Local Similarity 100.0%; Pred. No. 5.6e-95;
Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
DB 18 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
QY 61 SASFEPSNKGQTLVQVFTVKHEQNDICCGGVYKLPFNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SASFEPSNKGQTLVQVFTVKHEQNDICCGGVYKLPFNSLDQTMHGDSEYNIMFGPDIC 137

QY 121 GPGTKKVHVIENYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIENYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 8
US-10-316-253-2
; Sequence 2, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-2

Query Match 96.1%; Score 933; DB 14; Length 416;
Best Local Similarity 94.4%; Pred. No. 6.4e-91;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 EPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 60
DB 18 DPAYVFEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFYAL 77
QY 61 SASFEPSNKGQTLVQVFTVKHEQNDICCGGVYKLPFNSLDQTMHGDSEYNIMFGPDIC 120
DB 78 SARFEPSNKGQTLVQVFTVKHEQNDICCGGVYKLPFNSLDQTMHGDSEYNIMFGPDIC 137
QY 121 GPGTKKVHVIENYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 180
DB 138 GPGTKKVHVIENYKGNVINKDIRCKDDEFTHTLYTLIVRPDNTYEVKIDNSQVSGSLE 197

RESULT 9
US-10-316-253-4
; Sequence 4, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2002-12-10
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-4

Query Match 96.1%; Score 933; DB 14; Length 416;
Best Local Similarity 94.4%; Pred. No. 6.4e-91;
Matches 170; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

	Qy	1	EPAVTFKEQFLDGDGWTGRWIESRKHSDFGKFVLSSGKPYCGDBEKKGLQTSODARFYAL	60
	D5	:	: : :	:
	D5	18	DPAAVFKEQLDGDANTRWESRKHSDFGKFVLSSGKPYCQDKGLQTSODARFYAL	77
	Qy	61.	SASFPPFSNKGQTLLVQQTVTKHEQNIDCCGGYVKLFPNSLDQTMHGSDSYNIIMFGPDIC	120
	D5	78	SASFPPFSNKGQTLLVQQTVTKHEQNIDCCGGYVKLPFGLDQDMHGDSEYNIFMGPDIC	137
	Qy	121	GPCTKKGVHFINKGNVLINLRCKDDBFTHLYTLIVRPDNTYEYKVIDNSOVSGSUE	180
	D5	138	GPCTKKGVHFINKGNVLINLRCKDDBFTHLYTLIVRPDNTYEYKVIDNSOVSGSUE	197

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RESULT 10
US-10-316-253-6
; Sequence 6, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-6

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Query Match	96.1%	Score 933;	DB 14;	Length 416;
Best Local Similarity	94.4%;	Pred. No. 6.4e-91;		
Matches 170; Conservative	5;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	EPAVFYKQFIDGCGWTWRWIESKHSGDFGKFVLSGKYGDDEKDKGQTQSODARFVAL	60	
	:	:::::	:::::	
Db	18	DPAITFKQFIDGDAWNTNRWESKHSGDFGKFVLSGKYGDDEKDKGQTQSODARFVAL	77	
Qy	61	SASFPPFNKGOTLVVQFTVRHEQNIDCGGYVKLFNSLDQTDHMGDSEYNIIMGPDIC	120	
Db	78	SARPEPFNKGOTLVVQFTVRHEQNIDCGGYVKLFFGGILDQXDMHGDSYNIIMGPDIC	137	
Qy	121	GPGETKKVHVINYKGNVLNKDRCKDDBFTHYLTVIAPDNTYEVKTNDNSQVSFGSILE	180	
Db	138	GPGETKKVHVINYKGNVLNKDRCKDDBFTHYLTVIAPDNTYEVKTNDNSQVSFGSILE	197	

RESULT 11
US-10-161-927-46
; Sequence 46, Application US/10161927
; Publication No. US20030235821A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Miller, Charles E.
; APPLICANT: Hjal, Tordar
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Li, Li

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; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6343
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6343

Query Match      63.8%; Score 619.5; DB 14; Length 395;
Best Local Similarity 63.5%; Pred. No. 1.9e-57;
Matches 113; Conservative 26; Mismatches 36; Indels 3; Gaps 3;

QY  4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFVALSAS 63
Db  17 VYFKEFNDA-SWEKRWQSGKHDDFCAPKLSAGKFFDVESRDQGIQTSQDAKFYSRAAK 75

QY  64 FE-PFSGKQTLVQVFTVKHEQNIDCGGGYVKLPNSLDQTMHGDSEYNIMFGPDICGP 122
Db  76 FDKDFSNKGTLLVIQTVKHEQIDCGGGYVKMRADADLGDPHGTPTYNVMFGPDICGP 135

QY  123 GTKKVHVIFNYKGNVLINKDIRCKDETHLYTLVRPNTYEVKIDNSQVESGSL 180
Db  136 -TRRVHVLNKGKGLIKKEITCKSDDELTHLYTLNSDNTYEVKIDNSAQTGSL 192

RESULT 13
US-10-264-049-3546
; Sequence 3546, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133p1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patent in Ver. 3.1
; SEQ ID NO 3546
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: MISC FEATURE
; LOCATION: (138)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (149)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3546

Query Match      63.5%; Score 616.5; DB 15; Length 177;
Best Local Similarity 84.6%; Pred. No. 1.4e-57;
Matches 121; Conservative 3; Mismatches 18; Indels 1; Gaps 1;

QY  1 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFVAL 60
Db  29 EPVYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFVAL 88

QY  61 SASPEPFSNKGQTLVQVFTVKHEQNIDCGGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 119
Db  89 SASPEPFSNKGQTLVQVFTVKHEQNIDCGGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 148

QY  120 CGPCTKKVHVIFNYKGNVLINK 142
Db  149 XALAPKKVHVIFNYKGNGLINK 171

RESULT 14
US-10-767-701-55877

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; Sequence 55877, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5335)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 55877
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 30933722.pep
US-10-767-701-55877

Query Match      60.1%; Score 584; DB 16; Length 210;
Best Local Similarity 60.0%; Pred. No. 5.1e-54;
Matches 108; Conservative 30; Mismatches 36; Indels 6; Gaps 3;

QY  4 VYFKEQFLDGDG-WTSRWIES--XHKSDFGXFLVSSGKFGYDEEKDKGLQTSQDARFVAL 60
Db  26 VYFKETF---DGKWDRTWTESEWEACRGRKFAVTAAGFYNDDEADKGLQTTEDYRYITI 82

QY  61 SASPEPFSNKGQTLVQVFTVKHEQNIDCGGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 120
Db  83 SADHEEFSNKGKTLVLQYSLKNQKLDGCGGYLKFPPAGVDKKTGDSKYNIMFGPDIC 142

QY  121 GPGTKKHVIFNYKGNVLINKDIRCKDETHLYTLVRPNTYEVKIDNSQVESGSL 180
Db  143 GTTRKHVIFHEGKHLVKKEIPCETDETHLYTLVRPNTFEVLVDGSKATGSL 202

RESULT 15
US-10-425-114-70304
; Sequence 70304, Application US/10425114
; Publication No. US20040304888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70304
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMR0TEOSINTEL102C08_FLI.pep
US-10-425-114-70304

Query Match      55.2%; Score 536; DB 15; Length 435;
Best Local Similarity 56.4%; Pred. No. 1.8e-48;
Matches 101; Conservative 31; Mismatches 41; Indels 6; Gaps 3;

QY  4 VYFKEQFLDGDGWTSRWIESKHKSDFGKFLVSSGKFGYDEEKDKGLQTSQDARFVAL 60
Db  41 VYFKEP--EDWESRWYKSEKKDENWAGWHTSGKNGDAE-DKGIQISEYRFYAI 97

QY  61 SASPEPFSNKGQTLVQVFTVKHEQNIDCGGGYVKLPNSLDQTMHGDSEYNIMFGPDIC 120
Db  98 SAEYEPFSNKGKTLVLQFSVKHEQKLDGCGGYVKLLGGVDQKKFGGDTSYSIMFGPDIC 157

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Qy 121 GPCTKKVHVIFNYKGNVLINKDIRCKDDEFTHLYTLIVRPDNTYEVKIDNSQVESGSL 179
Db 158 GYSTKKVHTILTCKGNHLIKKDVPCETDQLTHVYTLIIRPDATYSILIDNEEKOTGSI 216

Search completed: October 15, 2004, 13:17:09
Job time : 49 secs